

05538

Delaval, Jan

From: Roark, Jessica
Sent: Wednesday, October 23, 2002 11:26 AM
To: Delaval, Jan
Subject: 09/728,420

Jan,

Please search, including pending, the following from 09/728,420:

SEQ ID NO:12
SEQ ID NO:7.

Please also align:

SEQ ID NO:17 and SEQ ID NO:18
SEQ ID NO:12 and SEQ ID NO:17
SEQ ID NO:12 and SEQ ID NO:13.

If you can do a pileup of all these sequences, with SEQ ID NO:12 as the reference, that would be great. If you can't do a pileup, then pairwise as indicated.

Results on paper please.

Thanks!

Jessica H. Roark

CM1 8A03
Mailbox 9E12
Art Unit 1644
703 605-1209

Jan Delaval
Reference Librarian
Biotechnology & Chemical Library
CM1 1E07 - 703-308-4498
jan.delaval@uspto.gov

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:16:41 ; Search time 29.0328 Seconds
(without alignments)
1231.909 Million cell updates/sec

Title: US-09-728-420C-7

Perfect score: 1687
Sequence: 1 MQLKCPFVSLGTROPVWKK.....RPHRSYTGPKTVQLELTDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

T number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : A_Geneseq_032802:*

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21: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1687	100.0	322	21	AA08725
2	1687	100.0	322	22	AA067711
3	1670	99.0	347	22	AA067712
4	1233.5	73.1	489	22	AA067719
5	600.5	35.6	302	22	AA087395
6	600.5	35.6	344	22	AA010504
7	600.5	35.6	344	22	AA018067
8	599.5	35.5	302	21	AA08729
9	599.5	35.5	302	22	AA067292
10	598.5	35.5	343	22	AA010322
11	598.5	35.5	345	22	AA010502

12	598.5	35.5	345	22	AA018065
13	598.5	35.5	370	22	AA018005
14	594.5	35.2	309	22	AA067713
15	592.5	35.1	516	22	AA004422
16	588.5	34.9	288	21	AA08727
17	569	33.7	239	22	AA004423
18	566.5	33.6	329	21	AA08730
19	558.5	33.1	490	22	AA067718
20	496	29.4	280	21	AA08728
21	249	14.8	316	22	AA00946
22	249	14.8	316	22	AA087394
23	247	14.6	316	20	AA041705
24	247	14.6	316	21	AA044261
25	247	14.6	316	22	AA029050
26	241.5	14.3	340	22	AA00904
27	241.5	14.3	388	22	AA03963
28	241.5	14.3	441	22	AA00905
29	241.5	14.3	534	22	AA000906
30	241.5	14.3	534	22	AA088459
31	241.5	14.3	534	22	AA087250
32	241.5	14.3	1020	22	AA039796
33	241	14.3	534	22	AA027249
34	240	14.2	533	22	AA03372
35	236.5	14.0	387	22	AA087415
36	235.5	14.0	469	22	AA041582
37	232.5	13.8	244	22	AA000949
38	227	13.5	216	22	AA000950
39	227	13.5	216	22	AA087417
40	192.5	11.4	133	22	AA067715
41	181	10.7	329	20	AA041076
42	180	10.7	313	19	AA034452
43	179	10.6	358	21	AA044414
44	177	10.5	309	16	AA067988
45	176.5	10.5	250	18	AA014944

ALIGNMENTS

RESULT 1	AA08725
ID	AA08725 standard; Protein: 322 AA.
XX	
AC	AA08725;
DT	02-JAN-2001 (first entry)
XX	
DE	Amino acid sequence of a murine B7RP1 polypeptide.
XX	
KW	CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
KW	T-lymphocyte activation; type I transmembrane protein; T cell
XX	T cell proliferation; T-cell mediated disorder.
XX	
OS	Mus sp.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..46
FT	/note= "signal peptide"
FT	47..322
FT	/note= "mature protein"
FT	47..279
FT	/note= "extracellular domain"
FT	280..298
FT	/note= "predicted transmembrane domain"
FT	299..322
FT	/note= "intracellular domain"
XX	
PD	WO200046240-A2.
XX	
PD	10-AUG-2000.
XX	
PF	27-JAN-2000; 2000WO-US01871.
XX	

Human immunoglobulin
Human immunoglobulin
Amino acid sequence
Human B7-3 protein
Amino acid sequence
Human B7-3 soluble
Amino acid sequence
Amino acid sequence
Human B7-H3 polypeptide
Human gene 2 encod
Human PRO352 prote
Human PRO352 (UNG3
Human PRO polypept
Human B lymphocyte
Human B lymphocyte
Human B lymphocyte
Human B lymphocyte
Human membrane or
Human amyloid prec
Human polypeptide
Human amyloid prec
Human polypeptide
Human gene 2 encod
Human gene 2 encod
Human polypeptide
Human B7-H3 polype
Human B7-H3 polype
Human gene 2 encod
Protein encoded by
Canine B7-2 protel
Rat CD86. Rattus
B7-2-beta 2 microg
Murine B lymphocyt
Chimeric human/por

PR 03-FEB-1999; 9905-0244448.
 PR 08-MAR-1999; 9905-0264527.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Yoshinaga SK;
 XX
 DR WPI: 2000-543476/49.
 DR N-PSDB; AAA64555.
 XX

PT Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT

Claim 12; Fig 2A; 174pp; English.

CC The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing, ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX

SQ Sequence 322 AA;

Query Match 100.0%; Score 1687; DB 21; Length 322;
 Best Local Similarity 100.0%; Pred. No. 2.3e-135;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 DB 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 QY 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPKRSPGINDVSSYKNGHSLDSMKGN 120
 DB 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPKRSPGINDVSSYKNGHSLDSMKGN 120
 QY 121 FSLYLNKNTVPDQTEFTCRVFMNTATLKYILIEVYRLRVANFSTPVISTSDSSNPQOE 180
 DB 121 FSLYLNKNTVPDQTEFTCRVFMNTATLKYILIEVYRLRVANFSTPVISTSDSSNPQOE 180
 QY 181 RYTTCMSKNGYPEPNLWYINTDNSLIDTALQNNVTYLNKLGIDVISTLRPLPMTSRGDV 240
 DB 181 RYTTCMSKNGYPEPNLWYINTDNSLIDTALQNNVTYLNKLGIDVISTLRPLPMTSRGDV 240
 DB 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFTIYR 300
 QY 301 RTRPHRSYTGPKTVQLELTDHA 322
 DB 301 RTRPHRSYTGPKTVQLELTDHA 322

RESULT 2

AAB67711
 ID AAB67711 standard; Protein; 322 AA.

AC AAB67711;

DT 11-JUN-2001 (first entry)

DE Amino acid sequence of a murine GL50-1.

KW GL50: antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine.

OS Mus musculus.
 XX

FH Key Location/Qualifiers
 FT Peptide 1..46
 FT /note="Leader sequence"
 FT Domain 47..279
 FT /note="extracellular domain"
 FT Region 280..298
 FT /note="hydrophobic transmembrane region"
 FT Domain 299..322
 FT /note="intracellular cytoplasmic domain"

WO200121796-A2.

29-MAR-2001.

21-SEP-2000; 2000WO-US25892.

21-SEP-1999; 9905-0155043.

(GEMV) GENETICS INST INC.

Ling V, Dunussi-Joannopoulos K;

WPI: 2001-244938/25.

N-PSDB; AAF79919.

New isolated nucleic acid encoding a GL50 polypeptide for modulating a
 immune response and reducing the proliferation of a tumour cell -

Claim 13; Fig 1; 195pp; English.

CC The present sequence represents a murine GL50-1 polypeptides. GL50
 CC molecules are antigens on the surface of antigen presenting cells,
 CC which costimulate T cell proliferation and bind to costimulatory
 CC receptor ligands on T cells. GL50 modulating agents are used to
 CC modulate an immune response in a subject. GL50 polypeptides are used
 CC to modulate T cell costimulation, and to reduce the proliferation of
 CC a tumour cell. Diseases that can be treated using GL50 molecules are
 CC graft-versus-host disease, autoimmune disease, allergies, acquired
 CC immune deficiency syndrome (AIDS), and viral infections. The GL50
 CC molecules can be used in vaccines. GL50 polynucleotides can be used
 CC to locate gene regions associated with genetic disease, in tissue
 CC typing, and in forensic identification of a biological sample.
 XX

SQ Sequence 322 AA;

Query Match 100.0%; Score 1687; DB 22; Length 322;
 Best Local Similarity 100.0%; Pred. No. 2.3e-135;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 DB 1 MQLKPCFVSLGTRQPVWKKLHVSSGFFSGIGLFLLLSLCAASAEFEVGMVGSNNYL 60
 QY 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPKRSPGINDVSSYKNGHSLDSMKGN 120
 DB 61 SCIDPHRRHFNLSGLVYVQIENPEVSVTYLLPKRSPGINDVSSYKNGHSLDSMKGN 120
 QY 121 FSLYLNKNTVPDQTEFTCRVFMNTATLKYILIEVYRLRVANFSTPVISTSDSSNPQOE 180
 DB 121 FSLYLNKNTVPDQTEFTCRVFMNTATLKYILIEVYRLRVANFSTPVISTSDSSNPQOE 180
 QY 181 RYTTCMSKNGYPEPNLWYINTDNSLIDTALQNNVTYLNKLGIDVISTLRPLPMTSRGDV 240
 DB 181 RYTTCMSKNGYPEPNLWYINTDNSLIDTALQNNVTYLNKLGIDVISTLRPLPMTSRGDV 240
 QY 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFTIYR 300
 DB 241 LCCVENVALHONITSISQAESEFTGNNTKNPQETHNNELKVLVPLVLAFAAFVSFTIYR 300
 QY 301 RTRPHRSYTGPKTVQLELTDHA 322
 DB 301 RTRPHRSYTGPKTVQLELTDHA 322

	RESULT	3
AAB67712	ID	AAB67712 standard; Protein: 347 AA.
XX	AC	AAB67712;
XX	DT	11-JUN-2001 (first entry)
XX	DE	Amino acid sequence of a murine GL50-2.
XX	KW	GL50; antigen; antigen presenting cell; T cell proliferation; tumour;
KM	graft-versus-host disease; autoimmune disease; allergy; viral infection;	
XX	acquired immune deficiency syndrome; AIDS; vaccine.	
OS	Mus musculus.	
PN	WO200121796-A2.	
XX	PD	29-MAR-2001.
XI	PB	21-SEP-2000; 2000WO-US25892.
PR	21-SEP-1999; 99US-0155043.	
PA	(GEMV) GENETICS INST INC.	
PI	Ling V, Dunussi-Joannopoulos K;	
DR	WPI; 2001-244938/25.	
DR	N-PSTDB; AAF79920.	
PT	New isolated nucleic acid encoding a GL50 polypeptide for modulating a	
PT	immune response and reducing the proliferation of a tumour cell -	
PS	Claim 13; Fig 2; 195pp; English.	
XX	The present sequence represents a murine GL50-2 polypeptides. GL50	
CC	molecules are antigens on the surface of antigen presenting cells,	
CC	which costimulate T cell proliferation and bind to costimulatory	
CC	receptor ligands on T cells. GL50 modulating agents are used to	
CC	modulate an immune response in a subject. GL50 polypeptides are used	
CC	to modulate T cell costimulation, and to reduce the proliferation of	
CC	a tumour cell. Diseases that can be treated using GL50 molecules are	
CC	graft-versus-host disease, autoimmune disease, allergies, acquired	
CC	immune deficiency syndrome (AIDS), and viral infections. The GL50	
CC	molecules can be used in vaccines. GL50 polynucleotides can be used	
CC	to locate gene regions associated with genetic disease, in tissue	
CC	typing, and in forensic identification of a biological sample.	
XX	Sequence 347 AA;	
SQ		
	Query Match	99.0%; Score 1670; DB 22; Length 347;
	Best Local Similarity	99.7%; Pred. No. 7.le-13;
	Matches 319; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
OY	1	MOLKPCPVSLGTROPVWKKLHVSAGFSGGLFLILLSSLCQAASAEFEVGAMGSNVVL 60
Dd	1	MOLKPCPVSLGTROPVWKKLHVSAGFSGGLFLILLSSLCQAASAEFEVGAMGSNVVL 60
OY	61	SCIDPBRHRHFNLGLLYVWQJENPEVSYTYLPPYKSPGINVDSSYKNRGHLSDSMKOCN 120
Dd	61	SCIDPBRHRHFNLGLLYVWQJENPEVSYTYLPPYKSPGINVDSSYKNRGHLSDSMKOCN 120
OY	121	FSLYIKANTPDOTGFCTRVEMNTATELVKILIEVVALRVANFSTPIVISTDSSNPGE 180
Dd	121	FSLYIKANTPDOTGFCTRVEMNTATELVKILIEVVALRVANFSTPIVISTDSSNPGE 180
OY	181	RYYCKMSKNGYPEPLNYLINFTDNLSLDITALQNNTVVYLNKLGIVIVISTLRLPMTSRGDV 240
Dd	181	RYYCKMSKNGYPEPLNYLINFTDNLSLDITALQNNTVVYLNKLGIVIVISTLRLPMTSHGDV 240
OY	241	LCCEVNVAHQNTISISGAESFTGNNTKPNPOETHNELKVLVPYLAIVLAAAEVFITYR 300

Db	241	LCCEENVVLHQNTTISQAESEFTGNTNPNQETHNNELKVLVPLVLAAMAAVSTIIR	300
Qy	301	RTRPNRSTGPKTVQLELTD	320
Db	301	RTRPNRSTGPKTVQLELTD	320
RESULT 4			
AAB67719	ID	AAB67719 standard; Protein; 489 AA.	
XX	AA	AAB67719;	
XX	DT	11-JUN-2001 (first entry)	
XX	DE	Amino acid sequence of mGL50-mIgG2m fusion protein.	
XX	KW	gI50; antigen; antigen presenting cell; T cell proliferation; tumour;	
KW	gI50; antigen; antigen presenting cell; T cell proliferation; tumour;		
KW	gI50; antigen; antigen presenting cell; T cell proliferation; tumour;		
KW	gI50; antigen; antigen presenting cell; T cell proliferation; tumour;		
XX	OS	Synthetic.	
XX	OS	Mus musculus.	
XX	PN	MO200121796-A2.	
XX	PD	29-MAR-2001.	
XX	PF	21-SEP-2000; 2000WO-US25892.	
XX	PR	21-SEP-1999; 99US-0155043.	
XX	PA	(GEMV) GENETICS INST INC.	
XX	PI	Ling V, Dunussi-Joannopoulos K;	
XX	DR	WPI: 2001-244938/25.	
XX	DR	N-PSDB; AAF79942.	
XX	PT	New isolated nucleic acid encoding a GL50 polypeptide for modulating a	
XX	PS	immune response and reducing the proliferation of a tumour cell -	
XX	PS	Disclosure; Fig 29B; 195pp; English.	
XX	CC	The present sequence represents a fusion protein, comprising murine GL50	
XX	CC	(mGL50) and murine IgG2a (mIgG2A). The fusion protein is used in the	
XX	CC	course of the invention. The specification describes GL50 polypeptides.	
XX	CC	GL50 molecules are antigens on the surface of antigen presenting cells,	
XX	CC	which costimulate T cell proliferation and bind to costimulatory receptor	
XX	CC	ligands on T cells. GL50 modulating agents are used to modulate an immune	
XX	CC	response in a subject. GL50 polypeptides are used to modulate T cell	
XX	CC	costimulation, and to reduce the proliferation of a tumour cell. Diseases	
XX	CC	that can be treated using GL50 molecules are graft-versus-host disease,	
XX	CC	autoimmune disease, allergies, acquired immune deficiency syndrome	
XX	CC	(AIDS), and viral infections. The GL50 molecules can be used in vaccines.	
XX	CC	GL50 polynucleotides can be used to locate gene regions associated with	
XX	CC	genetic disease, in tissue typing, and in forensic identification of a	
XX	CC	biological sample.	
XX	SO	Sequence 489 AA;	
XX	SO	Query Match 73.1%; Score 1233.5; DB 22; Length 489;	
XX	SO	Best Local Similarity 96.4%; Pred. No. 1.6e-96;	
XX	SO	Matches 239; Conservative 0; Mismatches 8; Indels 1; Gaps 1	
Qy	31	LGLEFLLLSSLCASAETEVGAMVGSNNVLSICIDPHRRHFWLSGLIYYWQIENPEVSVTY	90
Db	11	LSVIALDLFP-SMAKSETEVGAMVGSNNVLSICIDPHRRHFWLSGLIYYWQIENPEVSVTY	69
Qy	91	YLPRKSGINVDSSYNNRGLSLDSKKQNFSLYKANTPDQDTEFCRCVPMNTATELVK	150
Db	70	YLPRKSGINVDSSYNNRGLSLDSKKQNFSLYKANTPDQDTEFCRCVPMNTATELVK	129

CC	abnormalities, hematopoietic disorders, diseases of the immune system,
CC	AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
CC	allergies, neurological disorders (e.g., Alzheimer's disease,
CC	Parkinson's disease), cognitive disorders, schizophrenia, asthma,
CC	skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis,
CC	cardiovascular disorders, angiodysplasia, kidney disorders,
CC	gastrointestinal disorders, pregnancy-related disorders, endocrine
CC	disorders, and infections. The proteins can also be used to aid wound
CC	healing and epithelial cell proliferation, to prevent skin aging due to
CC	sunburn, to maintain organs before transplantation, for supporting cell
CC	culture of primary tissues, to regenerate tissues, to identify their
CC	cognate ligands or binding partners, and in chemotaxis, and can be used
CC	as a food additive or preservative to modify storage properties.
CC	Antibodies specific for a protein of the invention can be used in
CC	alleviating symptoms associated with the disorders mentioned above, and
CC	in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked
CC	immunosorbent assay (ELISA). The present sequence represents a human
CC	secreted protein of the invention.
CC	
XX	Sequence 302 AA:
XX	
XX	Query Match 35.6%; Score 600.5; DB 22; Length 302;
XX	Best Local Similarity 46.2%; Pred. No. 5,9e-43;
XX	Matches 140; Conservative 40; Mismatches 102; Indels 21; Gaps 8
QY	32 GLELLLSLCAASAELEGAMGWNVSLCIDPHRRHFNLSGLYVYMOIENPEVSITY 91
DB	7 GLLFLFLSLRADTQEKERVAMVSDVELSCAPBESRDLNDVYVYVYVYVYVYVYVYV 66
QY	92 LPKSPGIVNDSSYKNGRLSDSMKQGNFSLYKLVNTPDQTEFTCRVFNMTATLVKI 151
DB	67 IQNSLSLELVNDSRYRNRALAMPAGMLRGDFSLRLNVPVPODQKFCFLVLSQSLSGFEV 125
QY	152 LEEVRLRYAANFSPVISTSDSSNPGQ-ERYTQCSKSGDEPNLYWNTDNLSDIQA 210
DB	126 LEXEYTLINHAANFSPVYSAFHS--PSQDELFTFTCSINGYRPVNYWINKTIDNSLDDQA 183
QY	211 LQNTVYLVNKLGLDYVISTRLPMTSRGDLCCVENVALHQNITISQAESFTGNN--- 266
DB	184 LQNDVFLMRLGLDYVSVLRIARFSPVNIQCIENVLLQNMILTVGSG---TGNDIGER 239
QY	267 ---TNPQETHNNEL---KVLVPLVLAALAAAFVSFIYIRKTRPHRSTYGPXTV--QLEL 318
DB	240 DKITENPVSTGKNAATWSILAVLICLLVVAIVAGVCRDRCLQH-SYAGAAVSPETEL 298
QY	319 TDH 321
DB	299 TGH 301
XX	
XX	RESULT 6
XX	ABBI0504
XX	ID ABB10504 standard; Protein: 344 AA.
XX	CC ABB10504;
XX	DT 10-JAN-2002 (first entry)
XX	DE Human CDNA SEQ ID NO: 812.
XX	XX
XX	Human: gene therapy; neural disorder; immune system disorder;
KW	muscular disorder; reproductive disorder; gastrointestinal disorder;
KW	pulmonary disorder; cardiovascular disorder; renal disorder;
XX	proliferative disorder; inflammation.
XX	
XX	Homo sapiens.
XX	PN WO200154474-A2.
XX	PD 02-AUG-2001.
XX	PF 17-JAN-2001; 2001MO-US01349.
XX	

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:28:41 ; Search time 12.6689 Seconds
(without alignments)
620.817 Million cell updates/sec

Title: US-09-728-420C-7
Perfect score: 1687
Sequence: 1 MQLKPCFVSLGTROPVKK.....RPHSYTGPKIVQLDLDDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 segs, 24425594 residues
T number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents, AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	175.5	10.4	323	5	PCT-US94-09642-2
2	175.5	10.4	329	2	US-08-456-104-2
3	175.5	10.4	329	2	US-08-101-624-2
4	175.5	10.4	329	3	US-08-479-744A-2
5	175.5	10.4	329	4	US-08-280-757B-2
6	175.5	10.4	329	4	US-08-205-697A-23
7	175.5	10.4	329	4	US-08-702-525-23
8	175.5	10.4	329	4	US-08-403-253A-4
9	175.5	10.4	329	5	PCT-US95-02576-23
10	175.5	10.4	309	2	US-08-456-104-4
11	175.5	10.4	309	3	US-08-479-744A-23
12	175.5	10.4	309	4	US-08-280-757B-23
13	175.5	10.4	309	4	US-08-702-525-21
14	175.5	10.4	309	4	US-08-702-525-21
15	175.5	10.4	309	5	PCT-US95-02576-21
16	175.5	10.4	314	4	US-08-205-697A-13
17	175.5	10.4	314	4	US-08-702-525-13
18	175.5	10.4	314	5	PCT-US95-02576-13
19	162	9.6	473	4	US-09-171-945-131
20	160	9.5	288	2	US-08-147-772-2
21	160	9.5	288	2	US-08-456-104-6
22	160	9.5	288	2	US-08-101-624-23
23	160	9.5	288	2	US-08-751-767A-6
24	160	9.5	288	3	US-08-153-262-2
25	160	9.5	288	3	US-08-479-744A-29
26	160	9.5	288	4	US-08-280-757B-29
27	160	9.5	288	4	US-09-159-135-2

28	160	9.5	288	4	US-08-205-697A-19	Sequence 19, Appl
29	160	9.5	288	4	US-08-702-525-19	Sequence 19, Appl
30	160	9.5	288	4	US-09-450-798-2	Sequence 2, Appl
31	160	9.5	288	4	US-08-403-253A-2	Sequence 2, Appl
32	160	9.5	288	5	PCT-US95-02576-19	Sequence 19, Appl
33	151.5	9.0	589	2	US-08-724-394A-1	Sequence 1, Appl
34	150	8.9	208	4	US-09-460-384-36	Sequence 36, Appl
35	144.5	8.6	306	4	US-08-205-697A-17	Sequence 17, Appl
36	144.5	8.6	306	4	US-08-702-525-17	Sequence 17, Appl
37	144.5	8.6	306	5	PCT-US95-02576-17	Sequence 17, Appl
38	143.5	8.5	306	2	US-08-147-772-4	Sequence 4, Appl
39	143.5	8.5	306	2	US-08-456-104-8	Sequence 8, Appl
40	143.5	8.5	306	2	US-08-101-624-25	Sequence 25, Appl
41	143.5	8.5	306	3	US-08-153-262-4	Sequence 4, Appl
42	143.5	8.5	306	3	US-08-479-744A-31	Sequence 31, Appl
43	143.5	8.5	306	4	US-08-280-757B-31	Sequence 31, Appl
44	143.5	8.5	306	4	US-09-159-135-4	Sequence 4, Appl
45	143.5	8.5	306	4	US-09-450-798-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
PCT-US94-09642-2
Sequence 2, Application PC/TUS9409642

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
TITLE OF INVENTION: Protein and Related Reagents

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Schering-Plough Corporation, M-3-W
STREET: One Giralda Farms

CITY: Madison

STATE: New Jersey

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh IIcx

OPERATING SYSTEM: System Software 7.1

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09642

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/120,606

FILING DATE: 13-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/116,882

FILING DATE: 03-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.

REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0390K1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7398

TELEFAX: 201-822-7039

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-09642-2

Query Match 10.4%, Score 175.5; DB 5; Length 323;
Best Local Similarity 24.8%; Pred. No. 7.9e-08;
Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;
QY 30 GIGLELLLSLCAASAELEGAMGSMNVLSICDIPRRHRHNSGLIYVWQIENPEVSVT 89

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Db 2 GLSNILFVMAFLISGAAPLKIQAIFNETADLPQOFANSONQSLSELVVFQDQENLYLNE 61
QY 90 YLLPKSPGIVNDSSYKNGHLSLDSMKQGNFSLYKLVTPQDQEFYCFVFMNTATELV 149
Db 62 VYLG-KERFDSVHSKMYGRTSPDSDS-----WTLRLHNLQIKDKGLYCQCIHHKKPTGMI 115
QY 150 KILEEVLRLVAANFSTPYISTSDSSNPGQERTYTCMSKNGYPEP-NLWYINTDNLIL- 207
Db 116 RIHQMSSELVLANFSQPELVPISNTENYINLTCSSIHGYEPKMSVLLRTKNSTIE 175
QY 208 -DTALONNTYVYLNKGLYDVISTRLFPW---TSRGDVLCCVENVALHQNTISISQAESFT 263
Db 176 YDGIQKQSD--NVTELYDVISISVSFPDYISNMTIFCILET-----DKTRLSSPFSI- 228
QY 264 GNNTRKPOETHNNELKVLVPLVLAALAAVFSFIY-----RTRPRHSY-TGPKYV 314
Db 229 --ELEDPPPPDH-----IPWITAVLPVILICVWFCLIMKWKKKRPRNSYKCGINTM 281
315 QLE 317
282 ERE 284
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RESULT 2

```
US-08-456-104-2
; Sequence 2, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASED
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-2
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Query Match 10.4%; Score 175.5; DB 2; Length 329;
Best Local Similarity 24.8%; Pred. No. 8,1e-08;
Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

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QY 30 GLGLFLLLSLSCAASAEYEVGAMGNNVLSCIDPHRRHFLSLGYVYNOIENPEYSVT 89
Db 8 GLSNILFVMAFLISGAAPLKIQAIFNETADLPQOFANSONQSLSELVVFQDQENLYLNE 67
QY 90 YLLPKSPGIVNDSSYKNGHLSLDSMKQGNFSLYKLVTPQDQEFYCFVFMNTATELV 149
Db 68 VYLG-KERFDSVHSKMYGRTSPDSDS-----WTLRLHNLQIKDKGLYCQCIHHKKPTGMI 121
QY 150 KILEEVLRLVAANFSTPYISTSDSSNPGQERTYTCMSKNGYPEP-NLWYINTDNLIL- 207
Db 122 RIHQMSSELVLANFSQPELVPISNTENYINLTCSSIHGYEPKMSVLLRTKNSTIE 181
QY 208 -DTALONNTYVYLNKGLYDVISTRLFPW---TSRGDVLCCVENVALHQNTISISQAESFT 263
Db 182 YDGIQKQSD--NVTELYDVISISVSFPDYISNMTIFCILET-----DKTRLSSPFSI- 234
QY 264 GNNTRKPOETHNNELKVLVPLVLAALAAVFSFIY-----RTRPRHSY-TGPKYV 314
Db 235 --ELEDPPPPDH-----IPWITAVLPVILICVWFCLIMKWKKKRPRNSYKCGINTM 287
315 QLE 317
288 ERE 290
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RESULT 3

```
US-08-101-624-2
; Sequence 2, Application US/08101624
; Patent No. 5942607
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; TITLE OF INVENTION: NO. 5942607/EL CTLA4/CD28 Ligands and
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/101,624
; FILING DATE: 26-JUL-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-101-624-2
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Query Match 10.4%; Score 175.5; DB 2; Length 329;
Best Local Similarity 24.8%; Pred. No. 8,1e-08;
Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:27:51 ; Search time 16.3639 Seconds
(without alignments)
1890.790 Million cell updates/sec

Title: US-09-728-420C-7

Perfect score: 1687

Sequence: 1 MOLKPCFVSLGTRQPYWK.....RPHRSYTGPKTVQLELTDHA 322

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

T number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	184	10.9	330	2	146691
2	177	10.5	299	2	146690
3	176.5	10.5	275	2	146690
4	175.5	10.4	329	1	JC7604
5	175	10.4	309	2	149522
6	164	9.7	321	2	154766
7	160	9.5	288	2	A45803
8	151.5	9.0	526	2	S70587
9	146	8.7	289	2	G00031
10	145.5	8.6	487	2	S65133
11	145	8.5	526	2	A37821
12	144	8.5	309	2	149503
13	129	7.6	233	2	S29577
14	128.5	7.6	299	2	S56749
15	121	7.2	531	2	S06016
16	121	7.2	537	2	149769
17	120	7.1	537	2	A45815
18	119.5	7.1	646	2	138049
19	117.5	7.0	391	2	T09058
20	115.5	6.8	3707	2	S18252
21	115	6.8	662	2	T16525
22	114.5	6.8	549	2	S04845
23	114	6.8	1348	2	S51656
24	113	6.7	521	2	S34338
25	113	6.7	1106	1	PFHUGB
26	113	6.7	6642	1	T29757
27	112.5	6.7	509	2	JC5288
28	112.5	6.7	513	2	JC5289
29	112	6.6	503	2	JC5287

30	111.5	6.6	167	2	S29579	Ig light chain - r
31	111.5	6.6	1098	1	PFMSRB	platelet-derived g
32	111	6.6	583	2	T39428	album - human
33	110.5	6.6	588	2	JH0506	adhesion molecule
34	110.5	6.6	588	2	A45254	surface glycoprote
35	110	6.5	247	2	A55717	myelin/oligodentro
36	109.5	6.5	521	2	JC1508	biliary glycoprote
37	108	6.4	241	2	S69131	Ig heavy chain (DO
38	108	6.4	523	2	I50478	neurotin - goldfis
39	108	6.4	526	1	A32164	biliary glycoprote
40	107.5	6.4	587	2	JH0464	DM-GRASP precursor
41	106.5	6.3	588	2	T37202	B-CAM protein - hu
42	106	6.3	416	1	A42879	advanced glycosyla
43	106	6.3	1259	2	S36126	neural cell adhesi
44	105.5	6.3	228	2	S29575	Ig light chain - r
45	105.5	6.3	1694	2	S50065	staloachsin - mou

ALIGNMENTS

RESULT 1
146691
CD86 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_rev14-Feb-1997 #text_change 23-Jul-1999
C:Accession: 146691
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: 146689; M01D:95369849
A:Accession: 146691
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-330 <ISO>
A:Cross-references: GB:D49842; NID:g755098; PIDN:BA08642.1; PID:g755099
C:Superfamily: B7-2 antigen

Query Match 10.9%; Score 184; DB 2; Length 330;
Best Local Similarity 23.8%; Pred. No. 1.9e-06;
Matches 70; Conservative 53; Mismatches 137; Indels 34; Gaps 9;

QY	23	VSSGFFSGLGIFLLLSLCAASAFTEVGAMVGSNVYLSGIDPHRRFNLSGLYVMOIE 82
DB	1	MDACCTGLSVTFVFMALLSGAASLRIGAYFNKADLPQFTNSQSRSLSELVFMODQ 60
QY	83	NPEVSATYVYLPYKSPGINVDSSYKNRGHLSIDSMKQGFSLYLKNTPODTEFTGRVFM 142
DB	61	ERLVLYELFLGKREKPD-NVDPKTYIGR-----TSFDQSNMLQHLNVOIKKGYQCFVHH 114
QY	143	NTATELVKILIEEVRRLVNAANFSTPVISTSDSNPGQERTYTCMSKNGYEP-NLWIWINT 201
DB	115	RGAAGLVPIYQMSNELSVLANFQPEITLLSNITRNSAINMLTSSVOGYDEPKRMFVLK 174
QY	202	TDNS-----LIDFALDNNTYVYLNKLGIVYISLRLPWS--RGDLVGV-----ENVALH 250
DB	175	TENATTEYDGVIEKSQDNVT-----GLYNTISISGSTFSDDIRNATIVYLVOTESTET 228
QY	251	QNITSISOAESFTGNMTKNPDETHNNELKLVPLVLAALAAAFVSFT-IYRRT 303
DB	229	QHPPIYPAD-----PYVPEKPRMIAVAALTLIYVCGIYFLTLMKRKK 273

RESULT 2
146690
CD80 precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 14-Feb-1997 #sequence_rev14-Feb-1997 #text_change 29-Sep-1999
C:Accession: 146690
R:Isono, T.; Seto, A.
Immunogenetics 42, 217-220, 1995
A:Title: Cloning and sequencing of the rabbit gene encoding T-cell costimulatory mole
A:Reference number: 146689; M01D:95369849

A:Accession: I46690
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-299 <ISO>
 A:Cross-references: GB:D49843; NID:9755096; PIDN:BA008643.1; PID:9755097
 C:Superfamily: B-lymphocyte restricted antigen B7

Query Match 10.5%; Score 177; DB 2; Length 299;
 Best Local Similarity 25.8%; Pred. No. 5,7e-06;
 Matches 77; Conservative 42; Mismatches 120; Indels 60; Gaps 11;

QY 35 LLLSLCAASAEYEVGAMGVNVLSC-----IDPHRHFMISGLYVWQIENPEVSVT 89
 DB 22 LLAIAIHHSSGISQVTKSKEMALSCDYNISID-----ELARIRYWKQDOQNV--- 72
 QY 90 YLIPKSPGINVDSSYKNGHLSIDSMKQGNFSLYKNTPODQTEGTCRFVMTATELV 149
 DB 73 --LIIISGOVEWPEYKKNTPFDIIN---NLSMLALRLSDKGTTCVVKNGNSFR 126
 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEPMLYW-----IN 200
 127 REHLTSVTLISRADFPVPSITDIGHDPVVKR-IRCSASGCFPEPRPLAMDEGEELNAV 185
 QY 201 TTQNSLIDPALQNTYVYKLGIDYISTRLRPMTSRGDVLCCEVNAHONTISQAE 260
 DB 186 TTVDDQDDE-----LYSVSELDENVNTHNSIYCLIKRYGEL-----SVSOIF 228
 QY 261 SFTGNNTKPNQETHNNELK--VLVPLVLAFAAFVSFI-----YRRTPHRSYTG 310
 DB 229 PW-----SKRKQEPPIQLEFPWYIIPVSGALVLTAVVLYCLACRHVARKKRTIRNEETWG 283

RESULT 3

CD86 spliced variant CD86 deltaTM isoform - human
 C:Species: Homo sapiens (man)
 C>Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001
 C:Accession: J07604
 R:Magistrelli, G.; Caron, G.; Gauchat, J.F.; Jeanm, P.; Bonnefoy, J.Y.; Delneste, Y.
 Biochem. Biophys. Res. Commun. 280, 1211-1215, 2001
 A:Title: Identification of an alternatively spliced variant of human CD86 mRNA.
 A:Reference number: J07604; MUID:21092744; PMID:11162656
 A:Accession: J07604
 A:Molecule type: mRNA
 A:Residues: 1-275 <MAC>
 C:Comment: This CD86 variant expressed by activated human monocytes, is a costimulatory
 C:Genetics:
 A:Gene: cd86deltaTM
 Keywords: immune response

Query Match 10.5%; Score 176.5; DB 2; Length 275;
 Best Local Similarity 26.6%; Pred. No. 5,6e-06;
 Matches 73; Conservative 44; Mismatches 136; Indels 21; Gaps 8;

QY 30 GIGLFLILLSLCAASAEYEVGAMGVNVLSCIDPHRHFNLSGLYVWQIENPEVSVT 89
 DB 2 GLSNITLVMAFLISGAAPLKIQAIFNETADLPQOPANSQOSISELVFWQDOENVLNE 61
 QY 90 YLIPKSPGINVDSSYKNGHLSIDSMKQGNFSLYKNTPODQTEGTCRFVMTATELV 149
 DB 62 YVLG-KEKFDVSHKYMGTSPDS-----WTLRLHNLQIKKGLYQCIHHKKPTGMI 115
 QY 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEP-NLYWINTDMSLI- 207
 DB 116 RIHOMNSELVLANFSOPEIYVINSITENYINLTCSIHGPEPKKMSVLLRTKNSITE 175
 QY 208 -DTAQNNTYVYKLGIDYISTRLRPW---TSRGDVLCCEVNAHONTISQAESEFT 263
 DB 176 YDGMQKSD--NVTLEYDVISISVSFPDYTSNMTIFCILET-----DKTRLSSPFSI 228
 QY 264 GNNTKPNQETHNNEL--KVLVPLVLAFAAFVS 295
 DB 223 GNTMERESSEOTKKREKIHIPENSDERQVFKS 262

RESULT 4

A48754 B7-2 antigen - human
 N:Alternate names: B70 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A48754; S39055
 R:Freeman, G.O.; Gridben, D.G.; Boussetts, V.A.; Ng, J.W.; Restivo Jr., V.A.; Lombard
 Science 262, 909-911, 1993
 A:Title: Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T cell pr
 A:Reference number: A48754; MUID:94053735
 A:Accession: A48754
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-329 <FRET>
 A:Cross-references: GB:D25259; NID:9416368; PIDN:AAA58389.1; PID:9416369
 A>Note: It is uncertain whether Met-1 or Met-7 is the initiator
 R:Aizuma, M.; Ito, D.; Yagita, H.; Okumura, K.; Phillips, J.H.; Lanier, L.L.; Somoza,
 Nature 366, 76-79, 1993
 A:Title: B70 antigen is a second ligand for CTLA-4 and CD28.
 A:Reference number: S39055; MUID:94050123
 A:Accession: S39055
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 7-329 <AZU>
 A:Cross-references: GB:U04343; NID:9439838; PIDN:AAB03814.1; PID:9439839
 C:Genetics:
 A:Gene: GDB:CD86; CD28LG2
 A:Cross-references: GDB:433597; OMIM:601020
 A:Map position: 3q13.3-3q21
 C:Superfamily: B7-2 antigen
 C:Keywords: glycoprotein

Query Match 10.4%; Score 175.5; DB 1; Length 329;
 Best Local Similarity 24.8%; Pred. No. 8,4e-06;
 Matches 75; Conservative 51; Mismatches 142; Indels 35; Gaps 11;

QY 30 GIGLFLILLSLCAASAEYEVGAMGVNVLSCIDPHRHFNLSGLYVWQIENPEVSVT 89
 DB 8 GLSNITLVMAFLISGAAPLKIQAIFNETADLPQOPANSQOSISELVFWQDOENVLNE 67
 QY 90 YLIPKSPGINVDSSYKNGHLSIDSMKQGNFSLYKNTPODQTEGTCRFVMTATELV 149
 DB 68 YVLG-KEKFDVSHKYMGTSPDS-----WTLRLHNLQIKKGLYQCIHHKKPTGMI 121
 QY 150 KILEEYVRLVAAVFSTPVISTDSSNPGQERTYTCMSKNGYPEP-NLYWINTDMSLI- 207
 DB 122 RIHOMNSELVLANFSOPEIYVINSITENYINLTCSIHGPEPKKMSVLLRTKNSITE 181
 QY 208 -DTAQNNTYVYKLGIDYISTRLRPW---TSRGDVLCCEVNAHONTISQAESEFT 263
 DB 182 YDGMQKSD--NVTLEYDVISISVSFPDYTSNMTIFCILET-----DKTRLSSPFSI- 234
 QY 264 GNNTKPNQETHNNELKVLVPLVLAFAAFVSIIY-----RRTPRRSY-TGPKTV 314
 DB 235 --ELEDDQPPPDH-----IPWITAVLPTVILICWVCLIMKKKKKRPNSYKCGCTNM 287
 QY 315 QLE 317
 DB 288 ERE 290

RESULT 5

I49522 gene B7-2 protein - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Accession: I49522
 R:Freeman, G.J.; Borriello, F.; Hodes, R.J.; Reiser, H.; Gridben, J.G.; Ng, J.W.; Kim
 J. Exp. Med. 178, 2185-2192, 1993
 A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:23:41 ; Search time 9.50164 Seconds
(without alignments)
1312.163 Million cell updates/sec

Title: US-09-728-420C-7

Perfect score: 1687
Sequence: 1 MOLKCPFVSLGTRQPVNKK.....RPHRSYTGPKTVQLELTDHA 322

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1687	100.0	322	1 ICOL_MOUSE	09jh8 mus musculu
2	599.5	35.5	302	1 ICOL_HUMAN	075144 homo sapien
3	184	10.9	330	1 CD86_RABBIT	P42071 oryctolagus
4	177	10.5	299	1 CD80_RABBIT	P42070 oryctolagus
5	175.5	10.4	329	1 CD86_HUMAN	P42081 homo sapien
6	175	10.4	309	1 CD86_HUMAN	P42082 mus musculu
7	162	9.6	329	1 BUTY_MOUSE	062556 mus musculu
8	160	9.5	288	1 CD80_HUMAN	P33681 homo sapien
9	151.5	9.0	526	1 BUTY_HUMAN	013410 homo sapien
10	145	8.6	526	1 BUTY_BOVIN	P18892 bos taurus
11	144.5	8.6	306	1 CD80_MOUSE	000609 mus musculu
12	128.5	7.6	299	1 JAM1_HUMAN	09y624 homo sapien
13	121	7.2	537	1 ICAL_MOUSE	P13597 mus musculu
14	121	7.2	583	1 C166_MOUSE	061492 mus musculu
15	119.5	7.1	298	1 JAM2_HUMAN	P57087 homo sapien
16	119.5	7.1	646	1 MUI8_HUMAN	P43121 homo sapien
17	115.5	6.8	3707	1 PGBM_MOUSE	P57827 mus musculu
18	114	6.8	1348	1 VGR2_COTJA	P52583 coturnix co
19	113	6.7	1106	1 PGDR_HUMAN	P09619 homo sapien
20	111.5	6.6	555	1 C166_CARAU	090304 carassius a
21	111.5	6.6	1098	1 PGDR_MOUSE	P05622 mus musculu
22	111	6.6	583	1 C166_HUMAN	013740 homo sapien
23	110.5	6.6	246	1 MOG_MOUSE	061885 mus musculu
24	110.5	6.6	588	1 C166_CHICK	P42292 gallus gall
25	109.5	6.5	521	1 CEAL_MOUSE	P31809 mus musculu
26	108	6.4	319	1 A33_HUMAN	099795 homo sapien
27	108	6.4	526	1 CEAL_HUMAN	P13688 homo sapien
28	106	6.3	416	1 RAGE_BOVIN	028173 bos taurus
29	106	6.3	1259	1 CAML_RAT	005695 rattus norv
30	105.5	6.3	298	1 JAM1_BOVIN	09x156 bos taurus
31	105.5	6.3	1694	1 SN_MOUSE	062230 mus musculu
32	105	6.2	245	1 MOG_RAT	063345 rattus norv
33	104.5	6.2	313	1 HEMA_VARV	P33807 variola vir

34	104.5	6.2	421	1 EPC_MOUSE	P06336 mus musculu
35	104.5	6.2	569	1 TACT_HUMAN	P40200 homo sapien
36	104.5	6.2	730	1 ERG7_YEAST	P38604 saccharomyc
37	102.5	6.1	310	1 HEMA_RACVI	000716 raccoon pok
38	102.5	6.1	481	1 MUCM_ICMPU	P23735 ictalurus p
39	102	6.0	1709	1 SN_HUMAN	09b222 homo sapien
40	101.5	6.0	459	1 CD4_RABBIT	P46630 oryctolagus
41	101.5	6.0	1257	1 CAML_HUMAN	P32004 homo sapien
42	101	6.0	315	1 HEMA_VACCI	P08714 vaccinia vl
43	100	5.9	246	1 MOG_BOVIN	P55803 bos taurus
44	100	5.9	564	1 C166_BRARE	090460 brachydanio
45	99.5	5.9	628	1 LU_HUMAN	P50895 homo sapien

ALIGNMENTS

RESULT 1
ICOL_MOUSE
ID ICOL_MOUSE STANDARD; PRT; 322 AA.
AC 09JHJ8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
DE (B7-related protein-1) (B7Rp-1) (LICOS).
GN ICOSL OR B7H2 OR B7RPL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
OX NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RP TISSUE=Lymphocytes;
RC MEDLINE=20083495; PubMed=10617205;
RA Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
RA Horan T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shadlun A.,
RA Shalee C.L., Van G., Mak T.W., Senaldi G.,
RT "T-cell co-stimulation through B7Rp-1 and ICOS.";
RN Nature 402:827-832(1999).
[2]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP TISSUE=Thymus;
RC MEDLINE=20015817; PubMed=10549624;
RA Swallow M.M., Wallin J.J., Sha W.C.,
RT "B7, a novel costimulatory homolog of B7.1 and B7.2, is induced by
RT TNFalpha.";
RN Immunity 11:423-432(1999).
[3]
RN SEQUENCE FROM N.A. (ISOFORM 1).
RP STRAIN=C3H/HeJ; TISSUE=fetal thymus;
RC MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zoliner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.,
RT "Identification of G150, a novel B7-like protein that functionally
RT binds to ICOS receptor.";
RN J. Immunol. 164:1653-1657(2000).
[4]
RN SEQUENCE FROM N.A. (ISOFORM 2).
RP TISSUE=peripheral blood lymphocytes;
RC MEDLINE=21286479; PubMed=11390480;
RA Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
RA Collins M.,
RT "Differential expression of inducible costimulator-ligand splice
RT variants: lymphoid regulation of mouse g150-b and human g150
RT molecules.";
RN J. Immunol. 166:7300-7308(2001).
[5]
RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RA Ling V., Dunussi-Joannopoulos K.,

RT "G150 molecules and uses therefor.";
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
 CC PATCHES (MOSTLY IN THE FOLLICLES). LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYONISTS; IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC -----
 CC EMBL: AF216747; AAF45149.1; -
 CC EMBL: AF199027; AAF34738.1; -
 CC DR EMBL: AX100593; CAC36463.1; -
 CC DR EMBL: AX100593; CAC36464.1; -
 CC DR EMBL: AF394451; AAK77544.1; -
 CC DR MGD: MGI:1354701; Icosl.
 CC DR InterPro: IPR003599; Ig.
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR InterPro: IPR003600; Ig_Like.
 CC Pfam: PF00047; Ig_1.
 CC SMART: SM00409; Ig_1.
 CC SMART: SM00410; Ig_Like; 1.
 CC DR B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing.
 CC FT SIGNAL 1 46
 CC FT CHAIN 1 46
 CC FT DOMAIN 47 322
 CC FT TRANSMEM 278 298
 CC FT DOMAIN 299 322
 CC FT DOMAIN 55 145
 CC FT DOMAIN 178 250
 CC FT DOMAIN 31 38
 CC FT DOMAIN 289 292
 CC FT DISULFID 62 138
 CC FT DISULFID 185 243
 CC FT CARBOHYD 71 71
 CC FT CARBOHYD 120 120
 CC FT CARBOHYD 163 163
 CC FT CARBOHYD 200 200
 CC FT CARBOHYD 213 213
 CC FT CARBOHYD 252 252
 CC FT CARBOHYD 265 265
 CC FT VARSPLA 321 322

FT ISOFORM 2).
 FT CONFLICT 237 237 R -> H (IN REF. 4 AND 5; CAC36464).
 SQ SEQUENCE 322 AA; 35960 MW; 55CBA4AD12B47E6 CRC64;
 Query Match 100.0%; Score 1687; DB 1; Length 322;
 Best Local Similarity 100.0%; Pred. No. 3, 8e-129;
 Matches 322; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MQMKPCFVSGTGPVWKRIHVSSGFFSGIGLELLLSLCAASATFVGAWGSAVVL 60
 DB 1 MQLKCPFCVSLGTROPVWKRLHVSSGFFSGIGLELLLSLCAASATFVGAWGSAVVL 60
 QY 61 SCIPRRHFMFLSGIYYWQJENPEVSYTYLPPKSPGINVDSYKRGHLSDSMKG 120
 DB 61 SCIDPRHRHFMFLSGIYYWQJENPEVSYTYLPPKSPGINVDSYKRGHLSDSMKG 120
 QY 121 FSLYKLVNTPDQTEFCRCVFMNATATELVKILEEVRRLVAANSTPVISSDSSNGOE 180
 DB 121 FSLYKLVNTPDQTEFCRCVFMNATATELVKILEEVRRLVAANSTPVISSDSSNGOE 180
 QY 181 RTYCMKSNKGPENLVWINTDNLSDLTALQNTVYLNKLGIDVSTRLPWTSGDV 240
 DB 181 RTYCMKSNKGPENLVWINTDNLSDLTALQNTVYLNKLGIDVSTRLPWTSGDV 240
 QY 241 LCCVENVALHQNITISQAESFTGNNTKNPQETHNNELKVLVPLAVLAANAFTIYR 300
 DB 241 LCCVENVALHQNITISQAESFTGNNTKNPQETHNNELKVLVPLAVLAANAFTIYR 300
 QY 301 RTPRHRSYTGPKTVQLELTGHA 322
 DB 301 RTPRHRSYTGPKTVQLELTGHA 322
 RESULT 2
 ID ICOL_HUMAN STANDARD; PRT; 302 AA.
 AC 075144; Q9NR01; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)
 DE (B7-related protein-1) (B7Rp-1)
 GN ICOSL OR B7H2 OR B7Rp1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX MEDLINE=20477846; PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RT ICOS.";
 RL Blood 96:2808-2813(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX MEDLINE=20465019; PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
 RT "Characterization of a new human B7-related protein: B7Rp-1 is the
 RT ligand to the co-stimulatory protein ICOS.";
 RL Int. Immunol. 12:1439-1447(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=20126021; PubMed=10657606;
 RA Ling V., Wu P.W., Finmerly H.F., Bean K.M., Spaulding V., Fouser L.A.,
 RA Leonard J.P., Hunter S.E., Zoliner R., Thomas J.L., Miyashiro J.S.,
 RA Jacobs K.A., Collins M.;
 RT "Identification of G150, a novel B7-like protein that functionally

RT binds to ICOS receptor. [4]
 RL J. Immunol. 164:1653-1657(2000).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 Kotani H., Nomura N., Ohara O.;
 RT Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro. [5]
 RL DNA Res. 5:163-176(1998).
 RN
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Ling V., Dunussi-Joannopoulos K.;
 RT "G150 molecules and uses therefor."
 RL Patent number W00121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (by similarity).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
 CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
 CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,
 CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN
 CC LYMPH NODES, LEUKOCYTES AND SPLEEN.
 CC -1- INDICATION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
 CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
 CC MONOCYTES. WHILE IT IS DECREASED IN DENDRITIC CELLS.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300
 CC onward for an unknown reason.
 CC
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 CC
 CC EMBL; AF199028; AAF34739.1; -
 CC EMBL; AF289028; AAG01176.1; -
 CC EMBL; AF216749; AAK16241.1; -
 CC EMBL; AB014553; BAA31628.1; ALT-SEQ.
 CC EMBL; AX100595; CAC36465.1; -
 CC MIM; 605717; -
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR003600; Ig_Like.
 CC Pfam; PF00047; Ig_3.
 CC SMART; SM00409; Ig; 1.
 CC SMART; SM00410; Ig_Like; 1.
 CC B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing;
 FT SIGNAL 1 18 POTENTIAL.
 FT CHAIN 19 302 ICOS LIGAND.
 FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 257 277 POTENTIAL.
 FT DOMAIN 278 302 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 30 120 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 37 113 POTENTIAL.

FT DISULFID 158 216 POTENTIAL.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 300 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 302 302 GHV -> ESNMILLILS (IN ISOFORM 2).
 SQ SEQUENCE 302 AA; 33349 MW; 647934E21B5E34A CRC64;
 Query Match 35.5%; Score 599.5; DB 1; Length 302;
 Best Local Similarity 46.2%; Pred. No. 2,4e-41;
 Matches 140; Conservative 40; Mismatches 102; Indels 21; Gaps 8;
 QY 32 GLFLFLSSLCASAEETEGAMGNSVNLCDIPHRHFMLSGLYYWQIENDEVSVTYY 91
 DB 7 GLFLFLSSLRADQKEKVRAMVGSDELSCACPEGRFLNDVYYWQESSEKTYVTFH 66
 QY 92 LPYSPGINDSSKRNKNGHSLDSMKOGNSLYLKANTPDQDQEFRCRYMNTATLVKI 151
 DB 67 IPQSSLENDVSRNRNALMSPAGMLRGDFSLRFENVPDQEKFCGLV-LSSLSGFQEV 125
 QY 152 LEEVVRLLVAANFSTPYISTDSSNPGO-ERYTCMSKNGPPEPNLYWINTDNLIDTA 210
 DB 126 LSEVYTLHVAANFSPVYVSAFHS--PSQDELITFCISINGIPRPVYWKNTNSLDDA 183
 QY 211 LQNTVYLLKGLYDVISTRLPMTSRGDVLCVENYALHQNTSISQASFTGN--- 266
 DB 184 LQNTVFLNMHGLDYVSVLRIANTPVSNIQCCIEVLLQONLTVSGS---TGNDIGER 239
 QY 267 ---TKNPQETNNEL---KVLVPLVLAALAAAFVSFTIYKTRPRHRYTPKRY-QLEL 318
 DB 240 DKIEENPVSTGEKNAATWSILAVLCILVVAVALGWCRCRCLQH-SYAGAAVSPETEL 298
 QY 319 TDH 321
 DB 299 TGH 301
 RESULT 3
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE B lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 CX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHBB;HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules".
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:25:56 ; Search time 24.8098 Seconds
(without alignments)
2245.253 Million cell updates/sec

Title: US-09-728-420c-7
Perfect score: 1687
Sequence: 1 MOLKCPCEVSLGTRQPVWKK.....RPHRSYGTPTVQLTLDHA 322

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues
T number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP_RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_RVIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	365.5	21.7	296	13	042404	042404 gallus galli
2	246	14.6	316	4	Q9BXRI	Q9bxri homo sapien
3	181	10.7	329	6	Q9TTF2	Q9tft2 canis famli
4	180	10.7	309	11	Q91YV7	Q91yv7 mus musculu
5	180	10.7	313	11	Q35531	Q35531 ratu
6	178.5	10.6	356	11	Q64381	Q64381 mus musculu
7	175.5	10.4	323	6	Q9BDM9	Q9bdm9 macaca neme
8	175	10.4	314	11	Q61238	Q61238 mus musculu
9	175	10.4	325	6	Q02838	Q02838 sus scrofa
10	173.5	10.3	284	6	Q9GL33	Q9gl33 bos taurus
11	173	10.3	280	6	Q9TTF1	Q9tft1 canis famli
12	172.5	10.2	323	6	Q9BDM4	Q9bdm4 macaca mula
13	172.5	10.2	329	6	Q9XSX6	Q9xsx6 felis silve
14	172.5	10.2	332	6	Q9GMZ7	Q9gmz7 felis silve
15	172.5	10.2	332	6	Q9SL16	Q9sl16 felis silve
16	172	10.2	296	6	Q46405	Q46405 bos taurus

17	172	10.2	321	11	035187	035187 rattus norv
18	169.5	10.0	275	6	Q9BDN9	Q9bdn9 papio anubi
19	169.5	10.0	323	6	Q9BDB8	Q9bdb8 cercocobus
20	169	10.0	292	6	Q9GMZ8	Q9gmz8 felis silve
21	169	10.0	292	6	Q02758	Q02758 felis silve
22	167.5	9.9	323	6	Q9BDX2	Q9bdx2 cercopithec
23	165	9.8	288	6	Q28499	Q28499 macaca mula
24	165	9.8	290	4	Q9NZG7	Q9nzg7 homo sapien
25	164	9.7	321	11	Q62624	Q62624 rattus norv
26	160	9.5	524	11	Q921K7	Q921k7 mus musculu
27	158.5	9.4	290	11	Q62680	Q62680 rattus norv
28	158	9.4	288	6	Q77684	Q77684 macaca neme
29	158	9.4	304	6	Q9TQX1	Q9tqx1 canis famli
30	155	9.2	321	11	Q55202	Q55202 rattus norv
31	151.5	9.0	526	4	Q9H458	Q9h458 homo sapien
32	150	8.9	149	11	Q62810	Q62810 rattus norv
33	148	8.8	288	6	Q9TTF7	Q9tft7 sus scrofa
34	148	8.8	297	6	Q9BE99	Q9be99 sus scrofa
35	147.5	8.7	306	11	Q9R1Z9	Q9r1z9 mus musculu
36	147.5	8.7	584	4	Q00478	Q00478 homo sapien
37	146	8.7	288	6	Q9BDN6	Q9bdn6 cercocobus
38	146	8.7	289	6	Q28347	Q28347 cercocobus
39	144.5	8.6	235	6	Q9TOS8	Q9tgs8 canis famli
40	144.5	8.6	235	6	Q9N0R0	Q9n0r0 canis famli
41	142.5	8.4	290	11	Q9EP73	Q9ep73 mus musculu
42	142.5	8.4	319	4	Q00477	Q00477 homo sapien
43	142.5	8.4	334	4	Q9B081	Q9b081 homo sapien
44	142.5	8.4	357	4	Q15338	Q15338 homo sapien
45	142.5	8.4	359	4	P78410	P78410 homo sapien

ALIGNMENTS

RESULT 1	
042404	PRELIMINARY; PRT; 296 AA.
AC	042404
DT	01-JAN-1998 (TREMBLrel. 05, Created)
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE	CD80-LIKE PROTEIN.
OS	Gallus gallus (Chicken).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=WHITE LEHORN;
RA	O'Regan M.N.;
RT	"Chicken CD80 ligands."
RT	Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
DR	EMBL; Y08823; CAAT70058.1; -
DR	InterPro; IPR003599; IG_1ike.
DR	InterPro; IPR003600; IG_1MHC.
DR	Pfam; PF00047; IG_2.
DR	SMART; SM00409; IG_1like; 1.
DR	SMART; SM00410; IG_1like; 1.
DR	SEQUENCE 296 AA; 33155 MW; 061572FEB238C76 CRC64;
Query Match	21.7%; Score 365.5; DB 13; Length 296;
Best Local Similarity	35.6%; Pred. No. 1.7e-23;
Matches 106; Conservative 47; Mismatches 122; Indels 23; Gaps 10;	
QY	30 GIGLELLLSICASATEVGAWGVNVVSCIDPHRRHPLNSGLIVYWOIENPE--- 85
DB	5 GGFLFLPLHLIRAVTALEKTIISKRGDNATLSCIYAN-RGFDLDSLRYWQIDIVESSKS 63
QY	86 VSVVYLLLYKSPGIVVD--SSYKNGHLSLDKMGKGFSLYKNTVPDQTOEFCRVPMNT 144
DB	64 CSVVHALISGDNDSQCSQFRNRKTQLMDKLGDDPSLLLYNROSDEHTYKC-VVMQT 122

[illegible]

ID	Q9TFP2	PRELIMINARY;	PRT;	329 AA.
AC	Q9TFP2	01-MAY-2000 (Tremblrel. 13, Created)		
DT	01-MAY-2000 (Tremblrel. 13, Last sequence update)			
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)			
DE	B7-2 PROTEIN.			
GN	CD86.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20093996; PubMed=10630300;			
RA	Yang S., Sim G.-K.,			
RT	"New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7			
RT	Molecules."			
RL	Immunogenetics 50:349-353(1999).			
DR	EMBL; AF106826; AAF17297.1; -			
DR	InterPro: IPR003006; IG_MHC.			
DR	InterPro: IPR003596; IG_v.			
DR	SMART; SM00406; IGV; 1.			
DR	PROSITE; PS00290; IG_MHC; UNKNOWN.1.			
SQ	SEQUENCE 329 AA; 37774 MW; D98BB63437BF7B73 CRC64;			
Query Match	10.7%; Score 181; DB 6; Length 329;			
Best Local Similarity	26.1%; Pred. No. 1.5e-07;			
Matches	78; conservative 46; Mismatches 123; Indels 52; Gaps 13			
QY	33 LFLLLISLCAASAEETGVAGWGSNVLSCLDPHRRHNLGLIYYWQIENPEVSYTYL 92			
DB	13 LFLVMTLLTIGAAASMSQ--AYFNKGTGLPCHFTNSQNLISDELIVFWQDDKLVIYELXR 70			
QY	93 PKSGPINVDSSYKKNKGHLSDSMKGNFSILKNTPODQEPFCRVPMTATELYKL 152			
DB	71 GKENPD-NHKKRYKGR-----TSFDKDNWTLRLHNIQIKDKGLQCFYHHKGPGLVPMH 124			
QY	153 EEVYRLRYAANFTST-VISTSDSNPGDRTYTCMSKNQPEP-NLYWINTDNS--LLD 208			
DB	125 QANSLDVLNAPSOPEIWNSTNRTENSGIINLTCSIGCPPEPKEMYFLVKTENSTKYD 184			
QY	209 TALL--QNNTVYLNLGLIYDVISL--RLPMTSRGDVLCVE-----NVALIGN 252			
DB	185 IYMKKSQNNVT-----ELIVNISLSFSYPEASNVISFVLQLESKRLPLPYNDIAHKR 239			
QY	253 ITSISQAESFTGNNTKNPQETHNNELKLVLPVLAVALAAAFSLIYRTTRPHRSYTCP 311			
DB	240 PL-----PGGDHIIIMIALMLVNLVILCGWVF--FLTLRRK--KKQPGP 279			
RESULT 4				
Q91YV7	PRELIMINARY;	PRT;	309 AA.	
AC	Q91YV7	01-DEC-2001 (Tremblrel. 19, Created)		
DT	01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DT	CD86 ANTIGEN.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Straussberg R.;			
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; BC013807; AAH13807.1; -			
SQ	SEQUENCE 309 AA; 34714 MW; 61593C49EFC0CE5 CRC64;			
Query Match	10.7%; Score 180; DB 11; Length 309;			
Best Local Similarity	23.8%; Pred. No. 1.7e-07;			
Matches	64; conservative 53; Mismatches 120; Indels 24; Gaps 8			

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:27:51 ; Search time 14.6361 Seconds
(without alignments)
1890.790 Million cell updates/sec

Title: US-09-728-420C-12

Perfect score: 1495

Sequence: 1 MRLSPGLFLFLFSSLRADT.....VAVAIGWVCRDCLQHSYAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	194.5	13.0	487	2 S65133	butyrophillin - mou
2	182	12.2	309	2 I49522	gene B7-2 protein
3	179	12.0	526	2 S70587	butyrophillin precu
4	171.5	11.5	275	2 J07604	CD86 spliced varia
5	171	11.4	526	2 A37821	butyrophillin - bov
6	165.5	11.1	329	1 A48754	B7-2 antigen - hum
7	164.5	11.0	288	2 A45803	B-cell-restricted
8	158	10.6	330	2 I46691	CD86 precursor - r
9	145.5	9.5	309	2 I49503	B-lymphocyte activ
10	142.5	9.5	289	2 G00031	B7 protein - red-c
11	140.5	9.4	321	2 I54766	B-lymphocyte activ
12	139	9.3	274	2 A47639	OX-2 membrane glyco
13	135	9.0	299	2 I46690	CD80 precursor - r
14	133.5	8.9	509	2 J05288	SHP substrate-1 pr
15	133.5	8.9	513	2 J05289	SHP substrate-1 pr
16	124	8.3	278	1 TDRTOX	OX-2 membrane glyco
17	123	8.2	333	2 A31923	amalgam protein pr
18	122	8.2	646	2 I38049	cell surface glyco
19	117.5	7.9	946	1 A47299	cor-related recept
20	115.5	7.7	1256	2 T03096	CD0 protein - rat
21	115	7.7	739	2 A41288	vascular cell adhe
22	114	7.6	647	2 B41288	vascular cell adhe
23	114	7.6	662	2 T16525	hypothetical prote
24	114	7.6	702	2 A36319	carcinoembryonic a
25	112	7.5	503	2 J05287	SHP substrate-1 pr
26	111.5	7.5	569	2 A46462	T cell activation
27	110	7.4	299	2 S56749	functional adhesio
28	109.5	7.3	928	2 S16385	macrophage colony-
29	108.5	7.3	1896	2 T08851	down syndrome cell

30	107	7.2	234	2 S14237	Ig kappa chain pre
31	107	7.2	1087	2 I51552	platelet-derived g
32	107	7.2	1098	1 PFM5RB	platelet-derived g
33	106	7.1	584	2 I50419	s-glycerin precuro
34	105.5	7.1	477	1 I73631	brain-derived neur
35	105.5	7.1	822	1 A56853	adhesion molecule
36	105	7.0	588	2 JH0506	adhesion molecule
37	105	7.0	588	2 A45254	surfacte glycoprote
38	104.5	7.0	246	2 A47712	myelin/Oligodendro
39	104	7.0	1051	2 A39712	kinase-like protei
40	103.5	6.9	976	1 TVMSMD	macrophage colony-
41	103	6.9	538	2 J02457	vascular cell adhe
42	103	6.9	739	2 JN0581	vascular cell adhe
43	102.5	6.9	1860	2 T18531	tractin - medica
44	102	6.8	351	2 S39603	class I histocompa
45	101.5	6.8	1091	2 A58532	glial cell membran

ALIGNMENTS

RESULT 1
S65133
butyrophillin - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
C:Accession: S65133
R:ishii, T.; Aoki, N.; Noda, A.; Adachi, T.; Nakamura, R.; Matsuda, T.
Biochim. Biophys. Acta 1245, 285-292, 1995
A:Title: Carboxy-terminal cytoplasmic domain of mouse butyrophillin specifically assoc
A:Reference number: S65133; MUID:96125722
A:Accession: S65133
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-487 <ISH>
A:Cross-references: GB:580642; NID:g1246078; PIDN:AAB5893.1; PID:g1246079

Query Match 13.0%; Score 194.5; DB 2; Length 487;
Best Local Similarity 31.6%; Pred. No. 5.6e-08;
Matches 65; Conservative 35; Mismatches 93; Indels 13; Gaps 9;

QY	25	VRAWGVS-DVELSCACPPGSRFLNDYVYWMQTSKTVYVYH1PONSLLENVDSRRNR 83	
DB	1	VLAIVGSDDAELTCGFSPNASSEYIELMPROT-RSTAVLLIRPGQEGQGM-TEYRGR 58	

QY	84	ALMSFAGMLRGDFSLRLFNVPPODEKFKCLVLSQSLGFQVLSVEYTLHYANFSVPV 143	
DB	59	ATLAAGLLDGRATLLIRDAVRFSDGGEYRCL-FKNDDFEE--AAVYLKVAAGSDPOI 114	

QY	144	SAPHSODELTFCTGTSINGYPRPNVYVINKTDN-SLIDQALQNDYVFLNMRGLDYVSV 202	
DB	115	SWT-VQENGEMLECTSSGWYPEPOVW-RTGNREMLPST--SDSKHMEGELTVAVS 169	

QY	203	LRIARTPSVNIQCIEENLLOONLTV 228	
DB	170	MMISDSIKMNSCCIQNTLLGQKEV 195	

RESULT 2
I49522
gene B7-2 protein - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C:Accession: I49522
R:Freeman, G.J.; Borriello, F.; Hodges, R.J.; Reiser, H.; Gribben, J.G.; Ng, J.W.; Kim
J. Exp. Med. 178, 2185-2192, 1993
A:Title: Murine B7-2, an alternative CTLA4 counter-receptor that costimulates T cell
A:Reference number: I49522; MUID:94065585
A:Accession: I49522
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I25606; NID:g432478; PIDN:AAA9770.1; PID:g432479

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:23:41 ; Search time 8.49836 Seconds
(without alignments)
1312.163 Million cell updates/sec

Title: US-09-728-420c-12
Perfect score: 1495
Sequence: 1 MRUGSPGLFLFSSLRADT.....VAVALGWCRDRCLOHSTAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
T number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1495	100.0	302	1	ICOL_HUMAN
2	588.5	39.4	322	1	ICOL_MOUSE
3	203	13.6	524	1	BURY_MOUSE
4	182	12.2	309	1	CD86_MOUSE
5	179	12.0	526	1	BURY_HUMAN
6	167	11.2	526	1	BURY_BOVIN
7	165.5	11.1	329	1	CD86_HUMAN
8	164.5	11.0	288	1	CD80_HUMAN
9	158	10.6	330	1	CD86_RABIT
10	151.5	10.1	306	1	CD80_MOUSE
11	139	9.3	274	1	OX2G_HUMAN
12	135	9.0	299	1	CD80_RABIT
13	145	8.3	278	1	OX2G_RAT
14	123	8.2	298	1	JAM2_HUMAN
15	123	8.2	333	1	AMAL_DROME
16	122	8.2	646	1	MU18_HUMAN
17	115	7.7	739	1	VCA1_HUMAN
18	114	7.6	702	1	CEA5_HUMAN
19	111.5	7.5	569	1	TACT_HUMAN
20	110	7.4	299	1	JAM1_HUMAN
21	109.5	7.3	978	1	KFMS_RAT
22	108.5	7.3	2012	1	DSGA_HUMAN
23	107	7.2	1087	1	PGDS_XENLA
24	107	7.2	1098	1	PGSR_MOUSE
25	105.5	7.1	300	1	JAM1_MOUSE
26	105.5	7.1	822	1	TRKB_HUMAN
27	105	7.0	588	1	CL66_CHICK
28	104.5	7.0	246	1	MOS_BOVIN
29	104	7.0	976	1	KFMS_MOUSE
30	104	7.0	1051	1	PTK7_CHICK
31	103	6.9	739	1	VCA1_HUMAN
32	100.5	6.7	517	1	PVRL_HUMAN
33	99.5	6.7	583	1	CL66_MOUSE

34	98.5	6.6	247	1	MOS_HUMAN	016653	homo sapien
35	98	6.6	245	1	MOS_RAT	063345	rattus norv
36	98	6.6	530	1	PVR2_MOUSE	P32507	mus musculu
37	98	6.6	2029	1	LAR_DROME	P16621	drosophila
38	97.5	6.5	298	1	JAM1_BOVIN	09156	bos taurus
39	97.5	6.5	629	1	LY9_MOUSE	001965	mus musculu
40	97.5	6.5	764	1	ICCR_DROME	008180	mus musculu
41	97	6.5	349	1	LACH_SCHAM	026474	schistocerc
42	96.5	6.5	339	1	CD1A_PIG	09x572	sus scrofa
43	96.5	6.5	515	1	PVR1_PIG	09q176	sus scrofa
44	96.5	6.5	1070	1	PTK7_HUMAN	013308	homo sapien
45	95	6.4	246	1	MOS_MOUSE	061885	mus musculu

ALIGNMENTS

RESULT 1
ICOL_HUMAN STANDARD; PRT; 302 AA.
ID ICOL_HUMAN
AC 075144; Q9NRQ1; Q9HD18;
DT 15-JUL-1999 (Rel. 38, Created)
DR 16-OCT-2001 (Rel. 40, Last sequence update)
DI 01-MAR-2002 (Rel. 41, Last annotation update)
DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GL50)
DE (B7-related protein-1) (B7RP-1).
GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Metazoa; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Dendritic cell;
RX MEDLINE=20477846; PubMed=11023515;
RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
RT ICOS.";
RL Blood 96:2808-2813(2000).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=20465019; PubMed=1100762;
RA Yoshinaga S.K., Zhang M., Piscillo J., Horan T., Khare S.D., Miner K.,
RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,
RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;
RT "Characterization of a new human B7-related protein: B7RP-1 is the
RT ligand to the co-stimulatory protein ICOS.";
RL Int. Immunol. 12:1439-1447(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RC TISSUE=Leukocyte;
RX MEDLINE=20126021; PubMed=10657606;
RA Ling V., Wu P.W., Finererty H.F., Bean K.M., Spaulding V., Fouser L.A.,
RA Leonard J.P., Hunter S.E., Zolner R., Thomas J.L., Miyashiro J.S.,
RA Jacobs K.A., Collins M.;
RT "Identification of GL50, a novel B7-1-like protein that functionally
RT binds to ICOS receptor.";
RL J. Immunol. 164:1653-1657(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98403880; PubMed=9734811;
RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
RA Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. X.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro.";
RL DNA Res. 5:169-176(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX Ling V., Dunussi-Joannopoulos K.;
RT "GL50 molecules and uses therefor.";

```

RL Patent number W00121796, 29-MAR-2001.
CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein (By similarity).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2;
CC ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
CC KIDNEY, LIVER, LUNG, PANCREAS, SKELETAL MUSCLE, BONE
CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUCOCYTES,
CC SPLEEN, THYMUS AND TONSIL). WHILE ISOFORM 2 IS DETECTED ONLY IN
CC LYMPH NODES, LEUCOCYTES AND SPLEEN.
CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -1- CAUTION: Ref.4 sequence differs from that shown in position 300
CC onward for an unknown reason.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF199028; AAF34739.1; -
DR EMBL: AF289028; AAG01176.1; -
DR EMBL: AF216749; AAK16241.1; -
DR EMBL: AB014553; BAA31628.1; ALT_SEQ.
DR EMBL: AX100595; CAC36465.1; -
DR MIM: 605717; -
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003600; Ig_Like.
DR Pfam: PF00047; Ig_3.
DR SMART: SM00409; Ig_1.
DR SMART: SM00410; Ig_Like_1.
KW B-cell activation; Immune response; Glycoprotein;
KW Immunoglobulin domain; Signal; Transmembrane; Multigene family;
KW Alternative splicing.
FT CHAIN 1 18
FT DOMAIN 19 302 POTENTIAL.
FT TRANSMEM 19 256 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 278 302 POTENTIAL.
FT DOMAIN 30 120 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 151 223 IG-LIKE V-TYPE DOMAIN.
FT DISULFID 37 113 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 158 216 POTENTIAL.
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPIC 300 302 GHV -> ESMNILLIS (IN ISOFORM 2).
SQ SEQUENCE 302 AA; 33349 MW; 647934E21B53E34A CRC64;

Query Match 100.0%; Score 1495; DB 1; Length 302;
Best Local Similarity 100.0%; Pred. No. 1,4e-122;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRGSGGLFLFLFSSLRADTQKEKVRAMVGSDELSCACPEGRSFDLNDVYVWQTSSEK 60
DB 1 MRGSGGLFLFLFSSLRADTQKEKVRAMVGSDELSCACPEGRSFDLNDVYVWQTSSEK 60


```

RA Ling V., Dunussi-Joannopoulos K.:
 RT "G150 molecules and uses therefor."
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION. INDICES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS; 1 (SHOWN HERE) AND 2/B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTX AND IN BOTH PRIMARY AND SECONDARY
 CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PETER'S
 CC PATCHES (MOSTLY IN THE FOLLICLES). LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, HEART, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS, T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC -1- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYONIC STAGE. IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF216747; AAF45149.1; -;
 DR EMBL: AF199027; AAF34738.1; -;
 DR EMBL: AX100591; CAC36463.1; -;
 DR EMBL: AX100593; CAC36464.1; -;
 DR EMBL: AE394451; AAK7544.1; -;
 DR MGD: MGI:1354701; Icosl.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003600; Ig_Like.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00409; Ig; 1.
 DR SMART: SM00410; Ig_Like; 1.
 KW B-cell activation. Immune response. Glycoprotein;
 KW Immunoglobulin domain. Signal; Transmembrane; Multigene family;
 KW Alternative splicing.
 FT SIGNAL 46
 FT CHAIN 1
 FT CHAIN 47 322
 FT DOMAIN 277 298
 FT TRANSEM 278 298
 FT DOMAIN 299 322
 FT DOMAIN 322 322
 FT DOMAIN 55 145
 FT DOMAIN 178 250
 FT DOMAIN 31 38
 FT DOMAIN 289 292
 FT DISULFID 62 138
 FT DISULFID 185 243
 FT CARBOHYD 71 71
 FT CARBOHYD 120 120
 FT CARBOHYD 163 163
 FT CARBOHYD 200 200
 FT CARBOHYD 213 213
 FT CARBOHYD 252 252
 FT CARBOHYD 265 265

FT VARSPPLIC 321 322 HA -> TWAPVYQDYLIPIRYLMSPLCKTRGLP (IN
 FT FT CONFLICT 237 237 ISOFORM 2).
 FT FT SEQUENCE 322 AA; 35960 MW; 55CBAAD12E47E6 CRC64;
 SQ
 Query Match 39.4%; Score 588.5; DB 1; Length 322;
 Best local similarity 46.6%; Pred. No. 7.7e-44;
 Matches 135; Conservative 39; Mismatches 97; Indels 19; Gaps 7;
 QY 7 GLEPFLFSLPADYOEKVRAMGSDVELSCACPEGSFRLDNDVYVYQTSSEKTVYTH 66
 DB 32 GLEPFLFSLPADYOEKVRAMGSDVELSCACPEGSFRLDNDVYVYQTSSEKTVYTH 91
 QY 67 IPONSLENDRTNRRLMSBAGLKDSELRFPNTPODEQFRLY-LSQSLGQEV 125
 DB 92 LPKSPGGINVSSYKRNHLSIDSKMGQNFSLYLNKNTPODTEQFQVFNATYELVKI 151
 QY 126 LSEVETLVAAAFSPVVASAPHS--PSODELFTCTCSINGPRPNVYINKTDSLDQA 183
 DB 152 LEEVRLRVAANFSTPVLSTDSNSPQO-ERTYTCMSKNGIPERLNTINTTDSLDTA 210
 QY 184 LQNDTVFLMGRGLDVSVLRIARTPSVNICCIENVLQOQNTLVGSG--TGNDIGER 239
 DB 211 LQNTTVLNLKGLVYDVTSLRLPWTSGDVLQVENVALLQNTTISQAEFTGNN---- 266
 QY 240 DKITNPVSTGEKNAATWSIIAIVCLLVYVAVALGWCRCQCLQH-STAG 288
 DB 267 ---TKNPQETHNNEL--KVLPVLAVALAAAFVSFIYRTRRHSRYTG 310
 RESULT 3
 BUTY_MOUSE STANDARD; PRT; 524 AA.
 ID BUTY_MOUSE
 AC Q62556; P97392;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Butyrophillin precursor (BT).
 GN BTNL1 OR BTN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129; TISSUE=Mammary gland;
 RX MEDLINE=97148936; PubMed=8995761;
 RA Ogg S.L., Komaragiri M.V.S., Mather I.H.:
 RT "Structural organization and mammary-specific expression of the
 RT butyrophillin gene".
 RL Mam. Genome 7:900-905(1996).
 RN [2]
 RP SEQUENCE OF 39-487 FROM N.A.
 RC TISSUE=Mammary gland;
 RX MEDLINE=96125722; PubMed=8541302;
 RA Ishii T., Aoki N., Noda A., Adachi T., Nakamura R., Matsuda T.:
 RT "Carboxy-terminal cytoplasmic domain of mouse butyrophillin
 RT specifically associates with a 150-kDa protein of mammary epithelial
 RT cells and milk fat globule membrane".
 RL Biochim. Biophys. Acta 1245:285-292(1995).
 CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
 CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
 CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
 CC MEMBRANE (BY SIMILARITY).
 CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
 CC ASSOCIATION WITH THE MILK-FAT GLOBULE MEMBRANE DURING LACTATION.
 CC -1- DEVELOPMENTAL STAGE: EXPRESSION INCREASES DURING THE LAST HALF OF
 CC PREGNANCY AND IS MAXIMAL DURING LACTATION.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxId=10090;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=94065585; PubMed=7504059;
RA	Freeman G.J., Bottiello F., Hodas R.J., Reiser H., Gitben J.G.,
RA	Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszlo G., Lombard L.A.,
RA	Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RT	"Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RT	T cell proliferation and interleukin 2 production.";
RN	J. Exp. Med. 178:2185-2192(1993).
RN	[2]
RP	SEQUENCE FROM N.A.
RC	STRAIN=129;
RC	MEDLINE=96094437; PubMed=7499829;
RA	Bortello F., Oliveira J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RT	"Differential expression of alternate mb7-2 transcripts.";
RT	J. Immunol. 155:5490-5497(1995).
RN	[3]
RP	SEQUENCE OF 7-309 FROM N.A.
RX	MEDLINE=94230971; PubMed=7513726;
RA	Chen C., Gault A., Shen L., Nabavi N.;
RT	"Molecular cloning and expression of early T cell costimulatory
RT	molecule-1 and its characterization as B7-2 molecule.";
CC	J. Immunol. 152:4929-4936(1994).
CC	-1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC	FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC	BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC	EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NATIVE T CELLS,
CC	SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC	CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC	-1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC	-1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
CC	-1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC	-----
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CC	or send an email to license@isb-sib.ch).
CC	-----
DR	EMBL; L25606; AAA97970.1; -;
DR	EMBL; U39456; AAC52334.1; -;
DR	EMBL; U39459; AAC52334.1; JOINED.
DR	EMBL; U39461; AAC52334.1; JOINED.
DR	EMBL; U39462; AAC52334.1; JOINED.
DR	EMBL; U39463; AAC52334.1; JOINED.
DR	EMBL; U39464; AAC52334.1; JOINED.
DR	EMBL; U39465; AAC52334.1; JOINED.
DR	EMBL; U39466; AAC52334.1; JOINED.
DR	EMBL; U39467; AAC52336.1; JOINED.
DR	EMBL; U39468; AAC52336.1; JOINED.
DR	EMBL; U39469; AAC52336.1; JOINED.
DR	EMBL; U39470; AAC52336.1; JOINED.
DR	EMBL; U39471; AAC52336.1; JOINED.
DR	EMBL; U39472; AAC52336.1; JOINED.
DR	EMBL; U39473; AAC52336.1; JOINED.
DR	EMBL; U39474; AAC52336.1; JOINED.
DR	EMBL; U39475; AAC52336.1; JOINED.
DR	EMBL; U39476; AAC52336.1; JOINED.
DR	EMBL; U39477; AAC52336.1; JOINED.
DR	EMBL; U39478; AAC52336.1; JOINED.
DR	EMBL; U39479; AAC52336.1; JOINED.
DR	EMBL; U39480; AAC52336.1; JOINED.
DR	EMBL; U39481; AAC52336.1; JOINED.
DR	EMBL; U39482; AAC52336.1; JOINED.
DR	EMBL; U39483; AAC52336.1; JOINED.
DR	EMBL; U39484; AAC52336.1; JOINED.
DR	EMBL; U39485; AAC52336.1; JOINED.
DR	EMBL; U39486; AAC52336.1; JOINED.
DR	EMBL; U39487; AAC52336.1; JOINED.
DR	EMBL; U39488; AAC52336.1; JOINED.
DR	EMBL; U39489; AAC52336.1; JOINED.
DR	EMBL; U39490; AAC52336.1; JOINED.
DR	EMBL; U39491; AAC52336.1; JOINED.
DR	EMBL; U39492; AAC52336.1; JOINED.
DR	EMBL; U39493; AAC52336.1; JOINED.
DR	EMBL; U39494; AAC52336.1; JOINED.
DR	EMBL; U39495; AAC52336.1; JOINED.
DR	EMBL; U39496; AAC52336.1; JOINED.
DR	EMBL; U39497; AAC52336.1; JOINED.
DR	EMBL; U39498; AAC52336.1; JOINED.
DR	EMBL; U39499; AAC52336.1; JOINED.
DR	EMBL; U39500; AAC52336.1; JOINED.
DR	EMBL; U39501; AAC52336.1; JOINED.
DR	EMBL; U39502; AAC52336.1; JOINED.
DR	EMBL; U39503; AAC52336.1; JOINED.
DR	EMBL; U39504; AAC52336.1; JOINED.
DR	EMBL; U39505; AAC52336.1; JOINED.
DR	EMBL; U39506; AAC52336.1; JOINED.
DR	EMBL; U39507; AAC52336.1; JOINED.
DR	EMBL; U39508; AAC52336.1; JOINED.
DR	EMBL; U39509; AAC52336.1; JOINED.
DR	EMBL; U39510; AAC52336.1; JOINED.
DR	EMBL; U39511; AAC52336.1; JOINED.
DR	EMBL; U39512; AAC52336.1; JOINED.
DR	EMBL; U39513; AAC52336.1; JOINED.
DR	EMBL; U39514; AAC52336.1; JOINED.
DR	EMBL; U39515; AAC52336.1; JOINED.
DR	EMBL; U39516; AAC52336.1; JOINED.
DR	EMBL; U39517; AAC52336.1; JOINED.
DR	EMBL; U39518; AAC52336.1; JOINED.
DR	EMBL; U39519; AAC52336.1; JOINED.
DR	EMBL; U39520; AAC52336.1; JOINED.
DR	EMBL; U39521; AAC52336.1; JOINED.
DR	EMBL; U39522; AAC52336.1; JOINED.
DR	EMBL; U39523; AAC52336.1; JOINED.
DR	EMBL; U39524; AAC52336.1; JOIN

OY 117 SQSLEGEVLSE-VTLHVAANFSPVVASPHSPSQ---DELTFCTSGINGPRPNVWI 172
 121 -GTETRYRVLIHQEQVVLASASQPILSGRINSYSTGEVTFSCRSNDGYPEPNVWI 179
 OY 173 NKTNSLLDALQNDYFLNMKRGIDYVSVLRARIPSVNIGCCIEVNLQNLIV---- 228
 180 NRIDNTRLSSDFNIT--QHPDGTYSVLSLTKVNATSDMLECFIEKNKVLQENTSANYTE 237
 OY 229 ----GSQTNDIGERDKITENPVGKNAATWSILAVCLIVVAVAAGWCRCRCIQ 283
 238 EMONGSSTG-----SHKDAKGGGCAQAAYVSVILMAFLVILCMLWRRRSFQ 288

RESULT 2

O9BXRL PRELIMINARY; PRT; 316 AA.
 AC O9BXRL
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 01-JUN-2001 (Tremblrel. 17, last sequence update)
 01-DEC-2001 (Tremblrel. 19, last annotation update)
 COSTIMULATORY MOLECULE.
 Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21163383; PubMed-11224528;
 RA Chappoval A.I., Ni J., Lau J.S., Malcox R.A., Files D.B., Liu D.,
 RA Dong H., Sica G.L., Zhu G., Tamada K., Chen L.,
 RT "b7-43: A costimulatory molecule for T cell activation and IFN-gamma
 production.";
 RL Nat. Immun. 2:269-274(2001).
 DR EMBL: AF302102; AAK15438.1;
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003598; Ig_C2.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_2.
 DR SMART: SM00409; Ig; 2.
 DR SMART: SM00408; IGC2; 2.
 DR SMART: SM00410; IG_Like; 2.
 KW Immunoglobulin domain.
 SQ SEQUENCE 316 AA; 33791 MW; FF97007F191CFCFAI CRC64;

Query Match

Best Local Similarity 31.1%; Score 294.5; DB 4; Length 316;
 Matches 93; Conservative 40; Mismatches 111; Indels 55; Gaps 11;

OY 2 RLGSFG-----LFLFLFSSLRADTQKEKVRAMVGSDELSCACPEGSFRDLNDV 50
 4 RRGSPGAGVHGAALGALWFCILGALVEQVPEDPVALVGTIDATLCCSPSPGFSIAQL 63
 DB 4 RRGSPGAGVHGAALGALWFCILGALVEQVPEDPVALVGTIDATLCCSPSPGFSIAQL 63
 OY 51 YVWMTSEKTVYTHIQNSSLEND--SRYRNRALMSPAKMLRGDSLRLENFTPODE 108
 64 NLTWQLDTRKQLV-----HSAEGDQGSAAANRALTALPDLLAOGNALSRLQORVAD 117
 OY 109 QKFHCLVLSLGEFVLEVEYTLHVAANFSPVVASPHSPSQ---DELTFCTSGING 163
 118 GSTCTCVSIRDS-----SAAVSLOYAAAPSKP--SMILEPKKDLRPGVTITTSSTRG 170
 OY 164 YPPPNVYW-----INKTNSLLDALQNDYFLNMKRGIDYVSVLRARIPSVNIGCCIE 218
 171 YPEAEVFMODGQGVPLTGNVTTISQ-----MANEGQLDVHSLRVVLGANGTYSCLVR 223
 OY 219 NVTLQONLTVGSGTGNIDIBRKITENPVSTGEKNAATWSILAVCLIVVAVAAGWC 277
 DB 224 NPVLQOD-AHGSVT-----ITGQPMTPPE--ALWVTGLSVCLIALVALAFVC 270

RESULT 3

O921K7

ID O921K7 PRELIMINARY; PRT; 524 AA.
 AC O921K7
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE SIMILAR TO BOTYRPHILIN, SUBFAMILY 1, MEMBER A1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC011497; AAH11497.1;
 SQ SEQUENCE 524 AA; 58433 MW; 6DEFEBC6191E224 CRC64;

Query Match

Best Local Similarity 14.0%; Score 209; DB 11; Length 524;
 Matches 65; Conservative 37; Mismatches 94; Indels 12; Gaps 8;

OY 22 EKEVRAMGSDVELSCACPEGSFRDLNDVYYVWMTSEKTVYTHIQNSSLENDVSR 81
 DB 36 QEPVALVGSDELTCGFSPPNASSRYMELMFROT-RSKAVLLYRDQOEGQOM-TEYR 93
 OY 82 NRALSPAGMLRGDFSLRFLFNVTPQDEQKHFHCLVLSLGEFVLEVEYTLHVAANFSPV 141
 DB 94 GRATATATGLDGRATILIRVRSDDGEYRCL-FKNDDEE--AAVILKAAVASSDP 149
 OY 142 VVSAPHSPODELFTCTSGINGPRPNVWINKTDN-SLDQALQNDYFLNMKRGIDYV 200
 DB 150 QISMT-VOENGEEMLECTSSGMYPEPQYQW--RTGNREMLPST--SESKHNEGLPTVA 204
 OY 201 SVLRARIPSVNIGCCIEVNLQNLIV 228
 DB 205 VSMNRDSSINMSSCIONILLGQKEY 232

RESULT 4

O9BDM2 PRELIMINARY; PRT; 323 AA.
 AC O9BDM2
 DT 01-JUN-2001 (Tremblrel. 17, Created)
 DT 01-JUN-2001 (Tremblrel. 17, last sequence update)
 DT 01-DEC-2001 (Tremblrel. 19, last annotation update)
 DE CD86 PROTEIN.
 OS Cercopithecus aethiops (Green monkey) (Griivet).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OX NCBI_TaxID=9534;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-21383618; PubMed-11491535;
 RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P.,
 RA Weiss W.R., Ansari A.A.;
 RT "Cloning, sequencing, and homology analysis of nonhuman primate
 Fas/Fas-ligand and co-stimulatory molecules.";
 RL Immunogenetics 53:315-328(2001).
 DR EMBL: AF344661; AAK37543.1;
 DR InterPro: IPR003599; Ig_
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00409; IG; 1.
 DR SMART: SM00406; IGv; 1.
 SQ SEQUENCE 323 AA; 37045 MW; 3E43152A8FD17267 CRC64;

Query Match

Best Local Similarity 12.4%; Score 185; DB 6; Length 323;
 Matches 68; Conservative 59; Mismatches 120; Indels 46; Gaps 13;

OY 7 GLFLFLF--SSLRADTQKEKVRAMVGSDELSCACPEGSFRDLNDVYYVWMTSEKTVY 64
 DB 2 GLINILFVMAFLISGAAPLKIQAIFENETADLPQAFANSONRSISLVLVEWQENQENLV 61

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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:16:41 ; Search time 25.9672 Seconds

(without alignments)
1231.909 Million cell updates/sec

Title: US-09-728-420c-12

Perfect score: 1495

Sequence: 1 MRLGSPGLFLFLFSSLRADT.....VAVAIGWCRCRCLQHSYAG 288

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

1: A_Geneseq_032802.*
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT.*
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16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1495	100.0	288	21	AA08727
2	1495	100.0	302	21	AA08729
3	1495	100.0	302	22	AA067292
4	1495	100.0	309	22	AA067713
5	1495	100.0	516	22	AA000422
6	1494	99.9	343	22	AA010322
7	1494	99.9	345	22	AA010502
8	1494	99.9	345	22	AA018005
9	1494	99.7	370	22	AA018005
10	1490	99.7	302	22	AA087395
11	1490	99.7	344	22	AA010504

12	1490	99.7	344	22	AA018067
13	1236	82.7	239	22	AA000423
14	1218	81.5	490	22	AA067718
15	588.5	39.4	322	21	AA080725
16	588.5	39.4	322	21	AA067711
17	588.5	39.4	347	22	AA067712
18	577	38.6	133	22	AA067715
19	559.5	37.4	489	22	AA067719
20	539	36.1	329	21	AA080730
21	490.5	32.8	280	21	AA080728
22	290.5	19.4	316	20	AA041705
23	290.5	19.4	316	21	AA041705
24	290.5	19.4	316	22	AA029050
25	290.5	19.4	316	22	AA000946
26	290.5	19.4	316	22	AA087394
27	273.5	18.3	534	22	AA000906
28	273.5	18.3	534	22	AA027249
29	273.5	18.3	534	22	AA027250
30	273	18.3	340	22	AA000904
31	273	18.3	441	22	AA000905
32	272.5	18.2	533	22	AA03372
33	272.5	18.2	534	22	AA088459
34	271	18.1	387	22	AA087415
35	271	18.1	388	22	AA03963
36	271	18.1	1020	22	AA039796
37	267.5	17.9	244	22	AA000949
38	251	16.8	469	22	AA041582
39	247	16.5	216	22	AA000950
40	247	16.5	216	22	AA087417
41	203	13.6	524	19	AA046488
42	203	13.6	524	20	AA067816
43	193.5	12.9	524	20	AA067815
44	185	12.4	329	21	AA032285
45	185	12.4	329	21	AA032278

ALIGNMENTS

RESULT 1	AA08727	standard; Protein; 288 AA.
ID	AA08727	
AC	AA08727;	
XX	02-JAN-2001	(first entry)
DT		
DE		Amino acid sequence of a human B7RP1 polypeptide.
XX		
KW	CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;	
KW	T-lymphocyte activation; type I transmembrane protein; T cell activation;	
XX	T cell proliferation; T-cell mediated disorder.	
XX		
OS	Homo sapiens.	
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..16
FT	/note= "signal peptide"	17..288
FT	Protein	/note= "mature protein"
FT	Domain	259..274
FT	/note= "predicted transmembrane domain"	275..302
FT	Domain	/note= "intracellular domain"
XX		
XX	WO200046240-A2.	
XX	10-AUG-2000.	
XX	27-JAN-2000;	2000WO-US01871.
XX	03-FEB-1999;	99US-0244448.
XX	08-MAR-1999;	99US-0264527.
PR		

Human immunoglobulin
Human B7-3 soluble
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Protein encoded by
Amino acid sequenc
Amino acid sequenc
Human PRO352 (UNC3
Human PRO polypept
Human B7-H3 polype
Human gene 2 encod
Human B lymphocyte
Human amyloid prec
Human amyloid prec
Human B lymphocyte
Human polypeptide,
Human membrane or
Human gene 2 encod
Human polypeptide
Human B7-H3 polype
Human polypeptide
Human gene 2 encod
Human B7-H3 polype
Human gene 2 encod
Mouse butyrophilin
Guinea pig butyrop
Feline CD86 (B7-2)
Cat CD86 (B7-2) 11

XX (AMGE-) AMGEN INC.
 PA Yoshinaga SK;
 PI WPI; 2000-543476/49.
 DR N-PSDB; AAA64556.
 XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 PS Claim 12; Fig 3A; 174pp; English.
 XX
 PS The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 SQ Sequence 288 AA;
 Query Match 100.0%; Score 1495; DB 21; Length 288;
 Best Local Similarity 100.0%; Pred. No. 6-130;
 Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSPGLFLFLFSSLRADTQEKVRAMGSDVELSCACPEGSRFDLNDVYVYWTSESK 60
 DB 1 MRGSPGLFLFLFSSLRADTQEKVRAMGSDVELSCACPEGSRFDLNDVYVYWTSESK 60
 QY 61 TVVTYTHIPQSSLENDVSRYNRAIMSPAGMLRGDFSLRLFNVTPODEQFHCILVLSQSL 120
 DB 61 TVVTYTHIPQSSLENDVSRYNRAIMSPAGMLRGDFSLRLFNVTPODEQFHCILVLSQSL 120
 QY 121 GFQEVLSVEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWKINDNSL 180
 DB 121 GFQEVLSVEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWKINDNSL 180
 QY 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOONTLVGSQTGNDIGERD 240
 DB 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOONTLVGSQTGNDIGERD 240
 QY 241 KITENPVSTGEKNAATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 DB 241 KITENPVSTGEKNAATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 RESULT 2
 ID AAB08729 standard; protein; 302 AA.
 XX
 AC AAB08729;
 DT 02-JAN-2001 (first entry)
 XX
 DE Amino acid sequence of a human B7RP1 polypeptide.
 KW CRP1; CD28 related protein-1; B7RP1; B7 related protein-1;
 KW T-lymphocyte activation; type I transmembrane protein; T cell activation;
 KW T cell proliferation; T-cell mediated disorder.
 XX
 OS Homo sapiens.
 XX
 FH Key
 FT Peptide 1..16 Location/Qualifiers
 FT Protein 17..302 "signal peptide"
 FT /note="polypeptide"
 XX

PN WO200046240-A2.
 XX 10-AUG-2000.
 PD 27-JAN-2000; 2000WO-US01871.
 PF 03-FEB-1999; 99US-0244448.
 PR 08-MAR-1999; 99US-0264527.
 XX (AMGE-) AMGEN INC.
 PA Yoshinaga SK;
 PI WPI; 2000-543476/49.
 DR N-PSDB; AAA64557.
 XX Novel nucleic acids encoding the proteins CRP-1 and B7RP1 are useful
 PT in the treatment, prevention and diagnosis of T cell mediated disorders
 PT
 PS Claim 12; Fig 12A; 174pp; English.
 XX
 PS The present sequence represents a B7RP1 (B7 related protein-1)
 CC polypeptide. The specification also describes a CRP1 (CD28 related
 CC protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
 CC activation, and represent a receptor-ligand pair. CRP1 and B7RP1 are
 CC predicted to be a type I transmembrane protein. The nucleic acids are
 CC useful for regulating T cell activation or proliferation in an animal.
 CC The polypeptides are useful for treating, preventing ameliorating or
 CC diagnosing a T-cell mediated disorder in an animal. They can also be
 CC used to identify test molecules that bind to the polypeptides.
 XX
 SQ Sequence 302 AA;
 Query Match 100.0%; Score 1495; DB 21; Length 302;
 Best Local Similarity 100.0%; Pred. No. 7e-130;
 Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSPGLFLFLFSSLRADTQEKVRAMGSDVELSCACPEGSRFDLNDVYVYWTSESK 60
 DB 1 MRGSPGLFLFLFSSLRADTQEKVRAMGSDVELSCACPEGSRFDLNDVYVYWTSESK 60
 QY 61 TVVTYTHIPQSSLENDVSRYNRAIMSPAGMLRGDFSLRLFNVTPODEQFHCILVLSQSL 120
 DB 61 TVVTYTHIPQSSLENDVSRYNRAIMSPAGMLRGDFSLRLFNVTPODEQFHCILVLSQSL 120
 QY 121 GFQEVLSVEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWKINDNSL 180
 DB 121 GFQEVLSVEVTLHVAANFSVPVVSAPHSPODELFTCTSTNGYPRPNVYWKINDNSL 180
 QY 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOONTLVGSQTGNDIGERD 240
 DB 181 DQALQNDTVFLNMRGLYDVSVLRIARTPSVNICCIENVLQOONTLVGSQTGNDIGERD 240
 QY 241 KITENPVSTGEKNAATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 DB 241 KITENPVSTGEKNAATWSILAVLCLLVVAVAIQWVCRCRCLQHSYAG 288
 RESULT 3
 ID AAG67292 standard; protein; 302 AA.
 XX
 AC AAG67292;
 DT 13-NOV-2001 (first entry)
 XX
 DE Amino acid sequence of a human hB7-H2 polypeptide.
 KW hB7-H2; T cell stimulator; immunosuppression; cancer; AIDS;
 KW congenital immune deficiency; cellular immune response;
 KW inflammatory condition; autoimmune disease; rheumatoid arthritis;
 KW multiple sclerosis; insulin-dependent diabetes mellitus.

XX	Homo sapiens.
OS	
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..21
FT	/note= "signal peptide"
FT	27..135
FT	/note= "Igv-like domain"
FT	Domain
FT	136..248
FT	/note= "IgC-like domain"
PX	
PN	MO200164704-AL.
PD	
XD	07-SEP-2001.
XP	
PF	02-MAR-2001; 2001WO-US06769.
XX	
PR	02-MAR-2000; 2000US-0186519.
XX	
PA	(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
X	
P	Chen L;
XX	
DR	WPI; 2001-514837/56.
DR	N-PDB; AAH7869, AAH7870.
XX	
PT	An isolated DNA encoding a hb7-H2 polypeptide, useful for treating
PT	cancer, AIDS, or autoimmune diseases (e.g. rheumatoid arthritis,
PT	multiple sclerosis or insulin-dependent diabetes mellitus) -
PS	
PS	Claim 2; Fig 1A; 50pp; English.
XX	
CC	The present sequence represents a human polypeptide, designated hb7-H2.
CC	The hb7-H2 polypeptide co-stimulates T cells. The hb7-H2 proteins and its
CC	variants are generally useful as immune response-stimulating
CC	therapeutics. For example, the polypeptides can be used for treatment
CC	of disease conditions characterized by immunosuppression, e.g., cancer,
CC	AIDS or AIDS-related complex, other virally or environmentally-induced
CC	conditions, and certain congenital immune deficiencies. They may also
CC	be employed to increase immune function that has been impaired by the
CC	use of radiotherapy or immunosuppressive drugs such as certain
CC	chemotherapeutic agents, and therefore are particularly useful when
CC	given in conjunction with such drugs or radiotherapy. The hb7-H2
CC	nucleic acid and polypeptide can be used to treat conditions
CC	involving cellular immune responses, e.g., inflammatory conditions
CC	(such as, for example, those induced by infectious agents including
CC	Mycobacterium tuberculosis or M. leprae), or other pathologic
CC	cell-mediated responses such as those involved in autoimmune diseases
CC	(e.g. rheumatoid arthritis), multiple sclerosis, or insulin-dependent
CC	diabetes mellitus).
XX	
SO	Sequence 302 AA:
Query Match	100.0%; Score 1495; DB 22; Length 302;
Best Local Similarity	100.0%; Pred. No. 7e-130;
Matches 288; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	1 MRGSPGLFLFLSSRLRATDQEKVRAMGVSEVLSKCAPGSGSRFDLNDYVVYQTSESK 60
Db	1 MRGSPGLFLFLSSRLRATDQEKVRAMGVSEVLSKCAPGSGSRFDLNDYVVYQTSESK 60
QY	TVVTYTHHPQSSLENDSDRYRRNALKSPGMGRGFSLRLFNVPYPDEOKFHCILVSQSL 120
Db	61 TVVTYTHHPQSSLENDSDRYRRNALKSPGMGRGFSLRLFNVPYPDEOKFHCILVSQSL 120
QY	GFEVLSEVETLVHAANFSVPVVASAPHSPODELFFCTCSINGYPRPVWYINKTDSL 180
Db	121 GFEVLSEVETLVHAANFSVPVVASAPHSPODELFFCTCSINGYPRPVWYINKTDSL 180
QY	DQALQNTVTLNRKGLDYVSVLTARFYSVAIGCCIENVLLOONTLYVGSQTGMDISERD 240
Db	121 GFCEVLSEVETLVHAANFSVPVVASAPHSPODELFFCTCSINGYPRPVWYINKTDSL 180
QY	DQALQNTVTLNRKGLDYVSVLTARFYSVAIGCCIENVLLOONTLYVGSQTGMDISERD 240
Db	181 DQALQNTVTLNRKGLDYVSVLTARFYSVAIGCCIENVLLOONTLYVGSQTGMDISERD 240

QY	241	KITENPVSTGKNAATWSILAVLCILVYVAVAGVNCDRCLQHSYAG	288
Db	241	KITENPVSTGKNAATWSILAVLCILVYVAVAGVNCDRCLQHSYAG	288
RESULT 4			
AA	AB67713		
ID	AA67713	standard; Protein; 309 AA.	
XX	AA67713;		
AC			
XX			
DE	11-JUN-2001	(first entry)	
XX			
DE		Amino acid sequence of a human GL50 polypeptide.	
XX			
KW	GL50; antigen; antigen presenting cell; T cell proliferation; tumour;		
KW	graft-versus-host disease; autoimmune disease; allergy; viral infection;		
KW	acquired immune deficiency syndrome; AIDS; vaccine.		
XX			
OS	Homo sapiens.		
PN	WO200121796-A2.		
XX			
PD	29-MAR-2001.		
XX			
PF	21-SEP-2000; 2000WO-US25892.		
XX			
PR	21-SEP-1999; 99US-0155043.		
XX			
PA	(GENY) GENETICS INST INC.		
XX			
PI	Ling V, Dunussi-Joannopoulos K;		
XX			
DR	WPI; 2001-244938/25.		
DR	N-PSDB; AAF79921.		
XX			
PT	New isolated nucleic acid encoding a GL50 polypeptide for modulating a		
PT	immune response and reducing the proliferation of a tumour cell -		
XX			
PS	Claim 13; Fig 8; 195pp; English.		
XX			
CC	The present sequence represents a human GL50 polypeptides. GL50		
CC	molecules are antigens on the surface of antigen presenting cells,		
CC	which costimulate T cell proliferation and bind to costimulatory		
CC	receptor ligands on T cells. GL50 modulating agents are used to		
CC	modulate an immune response in a subject. GL50 polypeptides are used		
CC	to modulate T cell costimulation, and to reduce the proliferation of		
CC	a tumour cell. Diseases that can be treated using GL50 molecules are		
CC	graft-versus-host disease, autoimmune disease, allergies, acquired		
CC	immune deficiency syndrome (AIDS), and viral infections. The GL50		
CC	molecules can be used in vaccines. GL50 polynucleotides can be used		
CC	to locate gene regions associated with genetic disease, in tissue		
CC	typing, and in forensic identification of a biological sample.		
XX			
SO	Sequence	309 AA;	
Query Match	100.0%;	Score 1495;	DB 22; Length 309;
Best Local Similarity	100.0%;	Pred. No. 7.2e-130;	
Matches	288; Conservative	0; Mismatches	0; Indels
			0; Gaps
			0;
QY	1	MRIGSPGLLFLLFSSLRADTQKEVRAMVGSVDELSCACPEGSRPDLNDVYVWQTSSEK	60
Db	1	MRIGSPGLLFLLFSSLRADTQKEVRAMVGSVDELSCACPEGSRPDLNDVYVWQTSSEK	60
QY	61	TYVYTHIRPNSSLENDVDSYRNRALMSPAGMLRGPFSLRLEFVNTQDDKFFCIYLSGL	120
Db	61	TYVYTHIRPNSSLENDVDSYRNRALMSPAGMLRGPFSLRLEFVNTQDDKFFCIYLSGL	120
QY	121	GRQEVLSVETLHVANFVPVVASPHPSQDELFFTCISINGYRPNVYVWINKTIDNSLL	180
Db	121	GRQEVLSVETLHVANFVPVVASPHPSQDELFFTCISINGYRPNVYVWINKTIDNSLL	180
QY	181	DQALNDVYFELMRGILYDVAVLRLARTPSVNIGCCIEENVLLQMLTVGSQGTNDIGERD	240

|||||
Db 181 DOALQNDTVFLNMRGLYDVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
QY 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
Db 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
RESULT 5
AAU00422
ID AAU00422 standard; Protein; 516 AA.
XX
AC AAU00422;
XX
DT 11-MAY-2001 (first entry)
XX
DE Human B7-3 protein.
XX
KW Human; B7-3; Inducible co-stimulator; ICOS; T_H-D; KIAA0653; CD28; T-cell; ICOS-mediated activity; IL-10 production; TH2 activity; Helicobacter pylori induced peptic ulcer; Crohn's disease; multiple sclerosis; type I diabetes mellitus; graft rejection; helminth infection; allergic disease.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Binding-site 49..56 /note= "Beta-strand C sequence useful in the design of inhibitors of the interaction of B7-3 with ICOS"
FT Binding-site 60..67 /note= "Beta-strand C' sequence useful in the design of inhibitors of the interaction of B7-3 with ICOS"
FT Binding-site 73..77 /note= "Beta-strand C" sequence useful in the design of inhibitors of the interaction of B7-3 with ICOS"
FT Binding-site 109..118 /note= "Beta-strand F sequence useful in the design of inhibitors of the interaction of B7-3 with ICOS"
FT Binding-site 121..134 /note= "Beta-strand G sequence useful in the design of inhibitors of the interaction of B7-3 with ICOS"
XX
PN WO200112658-A2.
PD 22-FEB-2001.
XX
XX 10-AUG-2000; 2000WO-GB03079.
XX
XX 11-AUG-1999; 99US-0148402.
XX
PA (ISIS-) ISIS INNOVATIONS LTD.
XX
PI Davis S;
XX
DR WPI; 2001-226547/23.
DR N-PSDB; AAS00423.
XX
PT New B7-3 polypeptides useful for modulating inducible co-stimulator protein and for treating ulcers, Crohn's disease, multiple sclerosis, diabetes mellitus, infections and allergic diseases
PT
XX
XX Claim 1; Page 68; 77pp; English.
XX
XX The present sequence represents a novel human B7-3 protein which acts as a ligand for inducible co-stimulator (ICOS) protein. The B7-3 protein previously referred to as T_H-D or KIAA0653 was considered by the 2 CC groups as being incomplete. The present inventor has determined the CC sequence to be complete and renamed the sequence as B7-3. Also described CC is a soluble form of B7-3 (AAU00423) which comprises the B7-3 signal to CC sequence and extracellular domain. The extracellular domain is shown to CC bind ICOS which is related to CD28 and expressed on T-cells. B7-3 CC polypeptides or its fragments are useful for identifying a substance

CC which interacts with the polypeptide or its fragment. B7-3 polypeptides, CC fragments, tetramer, an agent with an ability to affect B7-3 activity or CC a specific binding member are useful for modulating an ICOS-mediated CC activity of T-cells by modulating IL-10 production and TH2 activity, and CC for manufacturing a medicament for modulating an ICOS-mediated activity of T-cells. B7-3 polypeptides are useful for development of diagnostic, CC prophylactic and therapeutic agents for diseases such as Helicobacter CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type CC I diabetes mellitus, graft rejection, helminth infections, and allergic CC diseases.
XX
SQ Sequence 516 AA;
XX
Query Match 100.0%; Score 1495; DB 22; Length 516;
Best Local Similarity 100.0%; Pred. No. 1,5e-129;
Matches 288; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRLGSPGLLFLFFSLRADTQEKERVAVGSDVELSCACPEGSFEDINDVYVWQTSSEK 60
Db 1 MRLGSPGLLFLFFSLRADTQEKERVAVGSDVELSCACPEGSFEDINDVYVWQTSSEK 60
QY 61 TVVYTHIPQNSLLENVDSRYNRRLMSPAGMLRQDFSLRLFNVPQDEQFHCILYLSQSL 120
Db 61 TVVYTHIPQNSLLENVDSRYNRRLMSPAGMLRQDFSLRLFNVPQDEQFHCILYLSQSL 120
QY 121 GFOEVLSEVTLHVAANFSPVVSAPHSQSODELFTCTSSINGYPRPNVWINKTNSLL 180
Db 121 GFOEVLSEVTLHVAANFSPVVSAPHSQSODELFTCTSSINGYPRPNVWINKTNSLL 180
QY 181 DOALQNDTVFLNMRGLYDVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
Db 181 DOALQNDTVFLNMRGLYDVSVLRIRTPSVNIGCCIEENVLLQONLTVGSQTGNDIGERD 240
QY 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
Db 241 KITEPNVSTGEKNAAWTSLIAVLCLLVYVAIVAIGWCRDRCLQHSYAG 288
RESULT 6
ABBI0322
ID ABBI0322 standard; Protein; 343 AA.
XX
AC ABBI0322;
XX
DT 10-JAN-2002 (first entry)
XX
XX Human CDNA SEQ ID NO: 630.
XX
KW Human; gene therapy; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder; proliferative disorder; inflammation.
OS Homo sapiens.
XX
PN WO200154474-A2.
PD 02-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01349.
XX
PR 31-JAN-2000; 2000US-179065P.
PR 04-FEB-2000; 2000US-180628P.
PR 24-FEB-2000; 2000US-184664P.
PR 02-MAR-2000; 2000US-186350P.
PR 16-MAR-2000; 2000US-189874P.
PR 17-MAR-2000; 2000US-190076P.
PR 18-APR-2000; 2000US-198123P.
PR 19-MAY-2000; 2000US-205515P.
PR 07-JUN-2000; 2000US-209467P.
PR 28-JUN-2000; 2000US-214886P.
PR 30-JUN-2000; 2000US-215135P.
PR 07-JUL-2000; 2000US-21647P.

PR 07-JUL-2000; 2000US-216880P.
PR 11-JUL-2000; 2000US-217487P.
PR 14-JUL-2000; 2000US-218290P.
PR 26-JUL-2000; 2000US-220963P.
PR 26-JUL-2000; 2000US-220964P.
PR 14-AUG-2000; 2000US-224518P.
PR 14-AUG-2000; 2000US-224519P.
PR 14-AUG-2000; 2000US-225213P.
PR 14-AUG-2000; 2000US-225214P.
PR 14-AUG-2000; 2000US-225267P.
PR 14-AUG-2000; 2000US-225268P.
PR 14-AUG-2000; 2000US-225270P.
PR 14-AUG-2000; 2000US-225447P.
PR 14-AUG-2000; 2000US-225757P.
PR 14-AUG-2000; 2000US-225758P.
PR 14-AUG-2000; 2000US-225759P.
PR 18-AUG-2000; 2000US-226279P.
PR 22-AUG-2000; 2000US-226681P.
PR 22-AUG-2000; 2000US-226868P.
PR 22-AUG-2000; 2000US-227182P.
PR 23-AUG-2000; 2000US-227009P.
PR 30-AUG-2000; 2000US-228924P.
PR 01-SEP-2000; 2000US-229287P.
PR 01-SEP-2000; 2000US-229343P.
PR 01-SEP-2000; 2000US-229344P.
PR 01-SEP-2000; 2000US-229345P.
PR 05-SEP-2000; 2000US-229509P.
PR 05-SEP-2000; 2000US-229513P.
PR 06-SEP-2000; 2000US-230437P.
PR 06-SEP-2000; 2000US-230438P.
PR 08-SEP-2000; 2000US-231242P.
PR 08-SEP-2000; 2000US-231243P.
PR 08-SEP-2000; 2000US-231244P.
PR 08-SEP-2000; 2000US-231413P.
PR 08-SEP-2000; 2000US-231414P.
PR 08-SEP-2000; 2000US-232080P.
PR 08-SEP-2000; 2000US-232081P.
PR 12-SEP-2000; 2000US-231968P.
PR 14-SEP-2000; 2000US-232397P.
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PR 20-OCT-2000; 2000US-241808P.

PR 20-OCT-2000; 2000US-241809P.
PR 20-OCT-2000; 2000US-241826P.
PR 01-NOV-2000; 2000US-244617P.
PR 08-NOV-2000; 2000US-246474P.
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PR 08-NOV-2000; 2000US-246532P.
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PR 08-DEC-2000; 2000US-251990P.
PR 11-DEC-2000; 2000US-254097P.
PR 05-JAN-2001; 2001US-259678P.

(HUMA-) HUMAN GENOME SCI INC.
PA
XX
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476161/51.
DX N-PSDB; ABA06544.
DR
XX
XX Isolated nucleic acid molecule encoding an inflammation-associated
PT polypeptide is used in preventing, treating or ameliorating a medical
PT condition -
PT
XX
XX
XX Claim 11; SEQ ID NO: 630; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention.
XX
XX
SQ Sequence 343 AA;

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PR 05-JAN-2001: 2001US-259678P.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476161/51.
DR N-PSDB; ABA06724.
XX
PT Isolated nucleic acid molecule encoding an inflammation-associated
X polypeptide is used in preventing, treating or ameliorating a medical
X condition -
PS Claim 11; SEQ ID NO: 810; 859pp + Sequence Listing; English.
XX
XX The present invention provides human cDNAs, proteins and related genomic
CC DNAs. These can be used in the treatment of neural, immune system,
CC muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC renal and proliferative disorders and inflammation. The present sequence
CC is a protein of the invention.
XX
SQ Sequence 345 AA:
Query Match 99.9%; Score 1494; DB 22; Length 345;
Best Local Similarity 99.7%; Pred. No. 1e-129; 0; Indels 0; Gaps 0;
Matches 287; Conservative 1; Mismatches 0;

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Db 224 DOALQNDIVFLNMRGLDYDVSVLRITAPSYNIGCCIEENVLLQONLTVGSOTGNDIGERD 283
QY 241 KITEPNVSTGKRNATWSILAVLCLLVVAVAIQWCRDRCLQHSYAG 288
Db 284 KITEPNVSTGKRNATWSILAVLCLLVVAVAIQWCRDRCLQHSYAG 331
RESULT 8
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ID AAU18065 standard; Protein: 345 AA.
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AC AAU18065;
XX
DT 07-NOV-2001 (first entry)
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XX Human immunoglobulin polypeptide SEQ ID No 210.
XX
KW Immunoglobulin: signal transduction pathway protein; cancer;
KW antitense therapy; gene therapy; neurological disorder; renal disorder;
KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
KW reproductive disorder; immune system disorder; proliferative disorder;
XX
XX Homo sapiens.
XX
XX W0200155315-A2.
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XX 02-AUG-2001.
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PF 17-JAN-2001; 2001WO-US01326.
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PR	08-NOV-2000	2000US-0246476
PR	08-NOV-2000	2000US-0246477
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PR	11-DEC-2000;	2000US-0251990.
PR	05-JAN-2001;	2001US-0259678.
XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	

XX Rosen CA, Barash SC, Ruben SM:
 PI
 XX
 XX WPI: 2001-457725/49.
 DR N-PSDB; AAS28853.
 DR
 XX Isolated novel immunoglobulin polypeptide for monitoring the presence
 PT and progression of diseases and for diagnosis -
 PT
 XX Claim 11: SEQ ID No 210; 551pp; English.
 SS

CC Sequences AA117977-AA11807 represent immunoglobulin polypeptides of the
CC invention. The polypeptides and their associated polynucleotides can be
CC used to diagnose a pathological condition or a susceptibility to a
CC pathological condition in a subject by determining the presence or
CC absence of a mutation in a DNA sequence or determining the presence or
CC amount of expression of the protein. Alternatively the identification of
CC a binding partner to a sequence allows determination of changes in
CC protein activity. The sequences can be used as research tools for
CC receptors or other signal transduction pathway proteins that interact
CC with the polypeptides of the invention and can be used to treat, prevent
CC or diagnose various types of disorders such as neurological disorders,
CC cardiovascular disorders, gastrointestinal disorders, reproductive
CC disorders, immune system disorders, renal disorders, muscular disorders,
CC pulmonary disorders, proliferative disorders and cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at wipo.int/pub/published_pat_sequences.

SQ	Sequence	345 AA;
	Query Match	99.9%; Score 1494; DB 22; Length 345;
	Best Local Similarity	99.7%; Pred. No. 1e-129;
	Matches 287; Conservative	0; Mismatches 0; Indels 0; Gaps 0

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	44	MRGSGCLLFLLFSSLRADTOEKEYRVMGSDVELSCAPBESGRDLNDVYYWOTSESK	103
QY	61	TVVTVYHHPONSSLNVNDSRYNRRALMSPAGMLGDESLRFVNTQDDBOKHCICLVLSOL	128
	104	TVVTVYHHPONSSLEVNDSRYNRRALMSPAGMLGDESLRFVNTQDDBOKHCICLVLSOL	163
QY	121	GFQEVLSVETVTHVANSVYVYVAPSPODELTFQCISINGVPRPNVYVYVNTKDSNL	180

Db 164 GFEVLSIEVTLVAVANFSPVVSAPHSPQDELFTCTISNGYPPPNYWKNTDNL 223
QY 181 DQALQNDYFELNRRGLDYVSVLRIARFPSPVNGCCIEENVLLQONLTYSQGTNDIGERD 240
Db 224 DQALQNDYFELNRRGLDYVSVLRIARFPSPVNGCCIEENVLLQONLTYSQGTNDIGERD 283
QY 241 KITEENVYSGEKNAATWSILAVLCCLVYVAVAIGWYGRRCLOHSTAG 288
Db 284 KITEENVYSGEKNAATWSILAVLCCLVYVAVAIGWYGRRCLOHSTAG 331

RESULT 9
AAU18005
ID AAU18005 standard; Protein: 370 AA.
XX
AC AAU18005;
XX
DT 07-NOV-2001 (first entry)
XX
DP Human immunoglobulin polypeptide SEQ ID No 150.
XX
KW Immunoglobulin; signal transduction pathway protein; cancer;
KW antileukemia therapy; gene therapy; neurological disorder; renal disorder;
KW cardiovascular disorder; gastrointestinal disorder; pulmonary disorder;
KW reproductive disorder; immune system disorder; proliferative disorder;
KW muscular disorder.
XX
OS Homo sapiens.
XX
PN WO200155315-A2.
XX
PD 02-AUG-2001.
XX
PE 17-JAN-2001; 2001MO-US01326.
XX
PR 31-JAN-2000; 2000US-0179065.
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PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.

PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249269.
 PR 17-NOV-2000; 2000US-0249299.
 PR 17-NOV-2000; 2000US-0249300.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 03-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251868.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 PT WPI: 2001-457725/49.
 DR N-PSDB; AAS28793.
 XX
 PT Isolated novel immunoglobulin polypeptide for monitoring the presence
 PT and progression of diseases and for diagnosis -
 XX
 PS Claim 11; SEQ ID No 150; 551bp; English.
 XX
 XX Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the
 CC invention. The polypeptides and their associated polynucleotides can be
 CC used to diagnose a pathological condition or a susceptibility to a
 CC pathological condition in a subject by determining the presence or
 CC absence of a mutation in a DNA sequence or determining the presence or
 CC amount of expression of the protein. Alternatively the identification of
 CC a binding partner to a sequence allows determination of changes in
 CC protein activity. The sequences can be used as research tools for
 CC receptors or other signal transduction pathway proteins that interact
 CC with the polypeptides of the invention and can be used to treat, prevent
 CC or diagnose various types of disorders such as neurological disorders,
 CC cardiovascular disorders, gastrointestinal disorders, reproductive
 CC disorders, immune system disorders, renal disorders, muscular disorders,
 CC pulmonary disorders, proliferative disorders and cancer.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIFO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SO Sequence 370 AA:
 Query Match 99.9%; Score 1494; DB 22; Length 370;
 Best Local Similarity 99.7%; Pred. No. 1,le-129;
 Matches 287; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MRGSGGLFLFSSLRADTQKEVRAMGSGVELSCAPESGSRFLNDVYVWQTSSEK 60
 DB 69 MRGSGGLFLFSSLRADTQKEVRAMGSGVELSCAPESGSRFLNDVYVWQTSSEK 128
 QY 61 TTYVTYIIPNSSLENDVSYRNRBALMSPAGMRGPESTRLEFWVTQDDQKFCILVLSGL 120
 DB 129 TTYVTYIIPNSSLENDVSYRNRBALMSPAGMRGPESTRLEFWVTQDDQKFCILVLSGL 188
 QY 121 GQGEVLSEVTLHVANFESVPYVSAHPSPODELFTCTCSINGYRPPVNYWINKTDSNLL 180
 DB 189 GQGEVLSEVTLHVANFESVPYVSAHPSPODELFTCTCSINGYRPPVNYWINKTDSNLL 248

QY 181 DOALQNDYFELNMRGLYDVSVLRIARTPSVNICCIENVLLQONLTVGSQTDNIGERD 240
 DB 249 DOALQNDYFELNMRGLYDVSVLRIARTPSVNICCIENVLLQONLTVGSQTDNIGERD 308
 QY 241 KITENPVSTGEKNAAVTSILAVLCILVYVAVAGVWCHDRCLQHSYAG 288
 DB 309 KITENPVSTGEKNAAVTSILAVLCILVYVAVAGVWCHDRCLQHSYAG 356
 RESULT 10
 AAB87395
 ID AAB87395 standard; Protein; 302 AA.
 AC AAB87395;
 XX
 DT 22-MAY-2001 (first entry)
 XX
 DE Human gene 2 encoded secreted protein HMWDB84, SEQ ID NO:136.
 XX
 KW Human; secreted protein; proliferative disorder; cancer; tumour;
 KW foetal abnormality; developmental abnormality; haematopoietic disorder;
 KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
 KW inflammation; allergy; neurological disorder; Alzheimer's disease;
 KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;
 KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;
 KW cardiovascular disorder; angiotensin disorder; kidney disorder;
 KW gastrointestinal disorder; pregnancy-related disorder;
 KW endocrine disorder; infection; wound healing; vulnerability;
 KW cell culture; chemotaxis; food additive;
 KW binding partner identification.
 XX
 OS Homo sapiens.
 XX
 XX WO200118022-A1.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US24008.
 XX
 PR 03-SEP-1999; 99US-0152315.
 PR 03-SEP-1999; 99US-0152317.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI NI J, Baker KP, Birse CE, Fiscella M, Komatsu G, Rosen CA;
 PI Soppet DR, Young PE, Ehner R, Duan DR, Olsen HS, Lafleur DW;
 PI Moore PA, Shi Y, Wei Y, Florence KA;
 XX
 DR WPI: 2001-203081/20.
 DR N-PSDB; AAF91911.
 XX
 PT Nucleic acid molecules encoding human secreted proteins, used in
 PT preventing, treating or ameliorating a disorder, e.g. Alzheimer's and
 PT Parkinson's diseases and cancers -
 XX
 XX
 PS Claim 11; Page 564-565; 607bp; English.
 XX
 XX AAF91858-AAF91929 represent cDNAs corresponding to 52 human secreted
 CC protein genes, and AAB87342-AAB87413 represent the proteins they encode.
 CC AAB87414-AAB87454 represent human secreted protein fragments. The genes
 CC and their corresponding secreted proteins are useful for preventing,
 CC treating or ameliorating medical conditions, e.g., by protein or gene
 CC therapy. Pathological conditions can be diagnosed by determining the
 CC amount of the new protein in a sample or by determining the presence of
 CC mutations in the new genes. Specific uses are described for each of the
 CC 52 genes, based on the tissues in which they are most highly expressed,
 CC and include developing products for the diagnosis or treatment of
 CC proliferative disorders, cancer, tumours, foetal and developmental
 CC abnormalities, haematopoietic disorders, diseases of the immune system,
 CC AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,
 CC allergies, neurological disorders (e.g., Alzheimer's disease,
 CC Parkinson's disease), cognitive disorders, schizophrenia, asthma,

PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225477.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239335.
PR 13-OCT-2000; 2000US-0239337.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.

PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0251988.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPT, 2001-457725/49.
N-PSDB; AAS28855.

Isolated novel immunoglobulin polypeptide for monitoring the presence
and progression of diseases and for diagnosis -

Claim 11; SEQ ID NO 212; 551pp; English.

Sequences AAU17977-AAU18087 represent immunoglobulin polypeptides of the
invention. The polypeptides and their associated polynucleotides can be
used to diagnose a pathological condition or a susceptibility to a
pathological condition in a subject by determining the presence or
absence of a mutation in a DNA sequence or determining the presence or
amount of expression of the protein. Alternatively the identification of
a binding partner to a sequence allows determination of changes in
protein activity. The sequences can be used as research tools for
receptors or other signal transduction pathway proteins that interact
with the polypeptides of the invention and can be used to treat, prevent
or diagnose various types of disorders such as neurological disorders,
cardiovascular disorders, gastrointestinal disorders, reproductive
disorders, immune system disorders, renal disorders, muscular disorders,
CC pulmonary disorders, proliferative disorders and cancer.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 344 AA;
 SQ Query Match 99.7%; Score 1490; DB 22; Length 344;
 Best Local Similarity 99.7%; Pred. No. 2.4e-129;
 Matches 287; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MRLSGPGLFLFLFSLRADTQEKVRAMVGSDELSCACPEGSFRFDNDVYVWQTSSEK 60
 |||||||
 Db 43 MRLSGPGLFLFLFSLRADTQEKVRAMVGSDELSCACPEGSFRFDNDVYVWQTSSEK 102
 |||||||

Qy 61 TVVTHIPQNSSLENVDSRYRNRLMSPAGMLRGDFSLRLFNVTPODEQKHFHCLVLSQSL 120
 |||||||
 Db 103 TVVTHIPQNSSLENVDSRYRNRLMSPAGMLRGDFSLRLFNVTPODEQKHFHCLVLSQSL 162
 |||||||

Qy 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTFCTSIINGPRPNVWINKTNSLL 180
 |||||||
 Db 163 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTFCTSIINGPRPNVWINKTNSLL 222
 |||||||

181 DQALQNDVFLNMRGLDVVSVLRIRARTPSVNICCIEENVLLQONLTVGSQGTGNDIGERD 240
 |||||||
 223 DQALQNDVFLNMRGLDVVSVLRIRARTPSVNICCIEENVLLQONLTVGSQGTGNDIGERD 282
 |||||||

Qy 241 KITEPNVSTGEKNAATWSILAVICLLVVAVAIGWVCRDRCLOHSTAG 288
 |||||||
 Db 283 KITEPNVSTGEKNAATWSILAVICLLVVAVAIGWVCRDRCLOHSTAG 330
 |||||||

RESULT 13
 AAD00423
 ID AAD00423 standard; Protein: 239 AA.
 AC AAD00423;
 XX 11-MAY-2001 (first entry)
 XX DE Human B7-3 soluble form protein.
 XX KW Human: B7-3; Inducible co-stimulator; ICOS; T0-D; KIA0653; CD28;
 KW T-cell; ICOS-mediated activity; IL-10 production; TH2 activity;
 KW Helicobacter pylori induced peptic ulcer; Crohn's disease;
 KW multiple sclerosis; type I diabetes mellitus; graft rejection;
 KW helminth infection; allergic disease.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT Binding-site 49..56
 /note= "Beta-strand C sequence useful in the design of
 inhibitors of the interaction of B7-3 with ICOS"
 FT Binding-site 60..67
 /note= "Beta-strand C' sequence useful in the design of
 inhibitors of the interaction of B7-3 with ICOS"
 FT Binding-site 73..77
 /note= "Beta-strand C" sequence useful in the design of
 inhibitors of the interaction of B7-3 with ICOS"
 FT Binding-site 109..118
 /note= "Beta-strand F sequence useful in the design of
 inhibitors of the interaction of B7-3 with ICOS"
 FT Binding-site 121..134
 /note= "Beta-strand G sequence useful in the design of
 inhibitors of the interaction of B7-3 with ICOS"
 FT Misc-difference 239
 /note= "Encoded by AG"
 XX WO200112658-A2.
 XX 22-FEB-2001.
 XX 10-AUG-2000; 2000WO-GB03079.
 XX 11-AUG-1999; 99US-0148402.

PA (ISIS-) ISIS INNOVATIONS LTD.
 XX PI Davis S;
 XX DR WPI: 2001-226547/23.
 XX DR N-PSDB: AAS00424.
 PT New B7-3 polypeptides useful for modulating inducible co-stimulator
 PT protein and for treating ulcers, Crohn's disease, multiple sclerosis,
 PT diabetes mellitus, infections and allergic diseases
 XX PS Claim 9; Page 69; 77pp; English.
 CC The present sequence represents human B7-3 soluble form protein which
 CC acts as a ligand for inducible co-stimulator (ICOS) protein. The B7-3
 CC soluble form protein comprises the B7-3 signal sequence and
 CC extracellular domain. The extracellular domain is shown to bind ICOS
 CC which is related to CD28 and expressed on T-cells. The B7-3 protein
 CC (AAD00422) previously referred to as T0-D or KIA0653 was considered by
 CC the 2 groups as being incomplete. The present inventor has determined
 CC the sequence to be complete and renamed the sequence as B7-3. B7-3
 CC polypeptides or its fragments are useful for identifying a substance
 CC which interacts with the polypeptide or its fragment. B7-3 polypeptides,
 CC fragments, tetramer, an agent with an ability to affect B7-3 activity or
 CC a specific binding member are useful for modulating an ICOS-mediated
 CC activity of T-cells by modulating IL-10 production and TH2 activity, and
 CC for manufacturing a medicament for modulating an ICOS-mediated activity
 CC of T-cells. B7-3 polypeptides are useful for development of diagnostic,
 CC prophylactic and therapeutic agents for diseases such as Helicobacter
 CC pylori induced peptic ulcers, Crohn's disease, multiple sclerosis, type
 CC I diabetes mellitus, graft rejection, helminth infections, and allergic
 CC diseases.
 XX SQ Sequence 239 AA;
 SQ Query Match 82.7%; Score 1236; DB 22; Length 239;
 Best Local Similarity 100.0%; Pred. No. 4.4e-106;
 Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MRLSGPGLFLFLFSLRADTQEKVRAMVGSDELSCACPEGSFRFDNDVYVWQTSSEK 60
 |||||||
 Db 1 MRLSGPGLFLFLFSLRADTQEKVRAMVGSDELSCACPEGSFRFDNDVYVWQTSSEK 60
 |||||||

Qy 61 TVVTHIPQNSSLENVDSRYRNRLMSPAGMLRGDFSLRLFNVTPODEQKHFHCLVLSQSL 120
 |||||||
 Db 61 TVVTHIPQNSSLENVDSRYRNRLMSPAGMLRGDFSLRLFNVTPODEQKHFHCLVLSQSL 120
 |||||||

Qy 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTFCTSIINGPRPNVWINKTNSLL 180
 |||||||
 Db 121 GFOEVLSEVTLHVAANFSVPVVSAPHSPODELFTFCTSIINGPRPNVWINKTNSLL 180
 |||||||

Qy 181 DQALQNDVFLNMRGLDVVSVLRIRARTPSVNICCIEENVLLQONLTVGSQGTGNDIGERD 239
 |||||||
 Db 181 DQALQNDVFLNMRGLDVVSVLRIRARTPSVNICCIEENVLLQONLTVGSQGTGNDIGERD 239
 |||||||

RESULT 14
 AAB67718
 ID AAB67718 standard; Protein: 490 AA.
 AC AAB67718;
 XX 11-JUN-2001 (first entry)
 XX Amino acid sequence of hG150-miG2am fusion protein.
 XX G150; antigen; antigen presenting cell; T cell proliferation; tumour;
 KW graft-versus-host disease; autoimmune disease; allergy; viral infection;
 KW acquired immune deficiency syndrome; AIDS; vaccine.
 XX OS Synthetic.
 OS Homo sapiens.
 OS Mus musculus.

```

XX  WC0200121796-A2.
PN
XX
XX  29-MAR-2001.
PD
XX
XX  21-SEP-2000; 2000WO-US25892.
PF
XX  21-SEP-1999; 99US-0155043.
PR
XX  (GENY ) GENETICS INST INC.
PA
XX  Ling V, Dunnuss-Ioannopolulos K;
PI
XX  WPI; 2001-244938/25.
DR  N-PSDB; AAF79941.
XX
XX  New isolated nucleic acid encoding a GL50 polypeptide for modulating a
PT  immune response and reducing the proliferation of a tumour cell -
XX
XX  Disclosure; Fig 28B; 195pp; English.
PS
XX  The present sequence represents a fusion protein, comprising human GL50
CC  (hGL50) and murine IgG2a (mig2a). The fusion protein is used in the
CC  course of the invention. The specification describes GL50 polypeptides.
CC  GL50 molecules are antigens on the surface of antigen presenting cells,
CC  which costimulate T cell proliferation and bind to costimulatory receptor
CC  ligands on T cells. GL50 modulating agents are used to modulate T cell
CC  response in a subject. GL50 polypeptides are used to modulate T cell
CC  costimulation, and to reduce the proliferation of a tumour cell. Diseases
CC  that can be treated using GL50 molecules are graft-versus-host disease,
CC  autoimmune disease, allergies, acquired immune deficiency syndrome
CC  (AIDS), and viral infections. The GL50 molecules can be used in vaccines.
CC  GL50 polynucleotides can be used to locate gene regions associated with
CC  genetic disease, in tissue typing, and in forensic identification of a
XX  biological sample.
XX
XX  Sequence 490 AA;
SQ
Query Match 81.5%; Score 1218; DB 22; Length 490;
Best Local Similarity 96.3%; Pred. No. 5.4e-104;
Matches 237; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
QY 8 LLEFLFSSLRADTQEKVRRAMVSGDVELSCACPEGSFRLNDVYVWQTSSEKTVVYTH 67
D 14 VLALFPSMA--SMEKVRAMVSGDVELSCACPEGSFRLNDVYVWQTSSEKTVVYTH 71
QY 68 PONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPQDEKRFHCLVLSQSIGFQEVLS 127
E 72 PONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPQDEKRFHCLVLSQSIGFQEVLS 131
QY 128 VEVTLHVAANFSPVVSAPHSPQDELFTCTSTINGYPRPNVYWIKNKTONSLDQALQND 187
D 132 VEVTLHVAANFSPVVSAPHSPQDELFTCTSTINGYPRPNVYWIKNKTONSLDQALQND 191
QY 188 TVEFLNMGIDVYVSLRLARTPSYNIQCTENVLQONLTVGSOTGNDIERKKTENPV 247
D 192 TVEFLNMGIDVYVSLRLARTPSYNIQCTENVLQONLTVGSOTGNDIERKKTENPV 251
QY 248 STGEKN 253
D 252 STGEKN 257
XX
XX  RESULT 15
XX  AAB08725
ID  AAB08725 standard; Protein; 322 AA.
XX
XX  AAB08725;
AC
XX  02-JAN-2001 (first entry)
DT
XX  Amino acid sequence of a murine B7Rp1 polypeptide.
DE
XX

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```

KW  CRP1; CD28 related protein-1; B7Rp1; B7 related protein-1;
KM  T-lymphocyte activation; type I transmembrane protein; T cell activation;
KM  T cell proliferation; T-cell mediated disorder.
XX
XX  Mus sp.
OS
XX
XX  Key
FH  Peptide
FT  1..46
FT  /note= "signal peptide"
FT  47..322
FT  /note= "mature protein"
FT  47..279
FT  Domain
FT  /note= "extracellular domain"
FT  280..298
FT  /note= "predicted transmembrane domain"
FT  299..322
FT  Domain
FT  /note= "intracellular domain"
XX
XX  WO20046240-A2.
PN
XX
XX  10-AUG-2000.
PD
XX
XX  27-JAN-2000; 2000WO-US01871.
XX
XX  03-FEB-1999; 99US-0244448.
XX  08-MAR-1999; 99US-0264527.
XX
XX  (AMGE-) AMGEN INC.
PA
XX  Yoshinaga SK;
PI
XX  WPI; 2000-543476/49.
XX  N-PSDB; AAA64555.
DR
XX
XX  Novel nucleic acids encoding the proteins CRP-1 and B7Rp1 are useful
PT  in the treatment, prevention and diagnosis of T cell mediated disorders
PT
XX
XX  Claim 12; Fig 2a; 174pp; English.
PS
XX
XX  The present sequence represents a B7Rp1 (B7 related protein-1)
CC  polypeptide. The specification also describes a CRP1 (CD28 related
CC  protein-1) polypeptide. The polypeptides are involved in T-lymphocyte
CC  activation, and represent a receptor-ligand pair. CRP1 and B7Rp1 are
CC  predicted to be a type I transmembrane protein. The nucleic acids are
CC  useful for regulating T cell activation or proliferation in an animal.
CC  The polypeptides are useful for treating, preventing ameliorating or
CC  diagnosing a T-cell mediated disorder in an animal. They can also be
CC  used to identify test molecules that bind to the polypeptides.
XX
XX  Sequence 322 AA;
SQ
Query Match 39.4%; Score 588.5; DB 21; Length 322;
Best Local Similarity 46.6%; Pred. No. 4.6e-46;
Matches 135; Conservative 39; Mismatches 97; Indels 19; Gaps 7;
QY 7 GLLEFLFSSLRADTQEKVRRAMVSGDVELSCACPEGSFRLNDVYVWQTSSEKTVVYTH 66
D 32 GLLEFLFSSLRADTQEKVRRAMVSGDVELSCACPEGSFRLNDVYVWQTSSEKTVVYTH 91
QY 67 IPONSLENVDSRYNRRLAMSPAGMLRGDFSLRLFNVPQDEKRFHCLVLSQSIGFQEV 125
D 92 LPEKSPGIVNDSSYKRNKRLSLDSMKQGFSLYLNVPDQDETCVFMATATELVKT 151
QY 126 LSEVTLHVAANFSPVVSAPHSPQDELFTCTSTINGYPRPNVYWIKNKTONSLDQAL 183
D 152 LSEVTLHVAANFSPVVSAPHSPQDELFTCTSTINGYPRPNVYWIKNKTONSLDQAL 210
QY 184 LONDVFLNMGIDVYVSLRLARTPSYNIQCTENVLQONLTVGSOTGNDIERKKTENPV 239
D 211 LONNIVYLNKGLIDVYVSLRLARTPSYNIQCTENVLQONLTVGSOTGNDIERKKTENPV 266
QY 240 DKITTENPVSTGEKNATWISILAVLCLLVVVAALGWCRDRLQH-SYAG 288

```

Wed Oct 23 13:57:48 2002

us-09-728-420c-12.rag

Page 16

Db 267 ---TKNPOETHNNEL---KVLVPVLAVIAAAAFVFSFIYRRRPHRSYTG 310

Search completed: October 23, 2002, 13:29:41
Job time : 26.9672 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 23, 2002, 13:28:41 ; Search time 11.3311 Seconds
(without alignments)
620.817 Million cell updates/sec

Title: US-09-728-420c-12

Perfect score: 1495
Sequence: 1 MVLGSPGLFLFLFSLRADT.....VAVALGWCRDRLQHSYAG 288

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

T number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/1/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/1/1aa/6A.COMB.pep:*
4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCITUS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	182	12.2	309	2 US-08-456-104-4	Sequence 4, Appl1
2	182	12.2	309	4 US-08-479-744A-23	Sequence 23, Appl1
3	182	12.2	309	4 US-08-280-757B-23	Sequence 23, Appl1
4	182	12.2	309	4 US-08-205-697A-21	Sequence 21, Appl1
5	182	12.2	309	4 US-08-702-525-21	Sequence 21, Appl1
6	182	12.2	309	5 PCT-US95-02576-21	Sequence 21, Appl1
7	182	12.2	314	4 US-08-205-697A-13	Sequence 13, Appl1
8	182	12.2	314	4 US-08-702-525-13	Sequence 13, Appl1
9	182	12.2	314	5 PCT-US95-02576-13	Sequence 13, Appl1
10	173	11.6	589	2 US-08-724-394A-1	Sequence 13, Appl1
11	165.5	11.1	323	5 PCT-US94-09642-2	Sequence 1, Appl1
12	165.5	11.1	329	2 US-08-456-104-2	Sequence 2, Appl1
13	165.5	11.1	329	2 US-08-101-624-2	Sequence 2, Appl1
14	165.5	11.1	329	3 US-08-479-744A-2	Sequence 2, Appl1
15	165.5	11.1	329	4 US-08-280-757B-2	Sequence 2, Appl1
16	165.5	11.1	329	4 US-08-205-697A-23	Sequence 23, Appl1
17	165.5	11.1	329	4 US-08-702-525-23	Sequence 23, Appl1
18	165.5	11.1	329	5 PCT-US95-02576-23	Sequence 23, Appl1
19	165.5	11.1	329	5 PCT-US95-02576-23	Sequence 23, Appl1
20	164.5	11.0	288	2 US-08-147-772-2	Sequence 2, Appl1
21	164.5	11.0	288	2 US-08-456-104-6	Sequence 6, Appl1
22	164.5	11.0	288	2 US-08-101-624-23	Sequence 23, Appl1
23	164.5	11.0	288	2 US-08-751-767A-6	Sequence 6, Appl1
24	164.5	11.0	288	3 US-08-153-262-2	Sequence 6, Appl1
25	164.5	11.0	288	3 US-08-479-744A-29	Sequence 29, Appl1
26	164.5	11.0	288	4 US-08-280-757B-29	Sequence 29, Appl1
27	164.5	11.0	288	4 US-09-159-135-2	Sequence 2, Appl1

28	164.5	11.0	288	4 US-08-205-697A-19	Sequence 19, Appl1
29	164.5	11.0	288	4 US-08-702-525-19	Sequence 19, Appl1
30	164.5	11.0	288	4 US-09-450-798-2	Sequence 2, Appl1
31	164.5	11.0	288	4 US-08-403-253A-2	Sequence 2, Appl1
32	164.5	11.0	288	5 PCT-US95-02576-19	Sequence 19, Appl1
33	161	10.8	208	4 US-09-460-384-36	Sequence 36, Appl1
34	161	10.8	473	4 US-09-171-945-131	Sequence 131, Appl1
35	158	10.6	208	3 US-08-630-172-15	Sequence 15, Appl1
36	158	10.6	208	4 US-09-375-419-15	Sequence 15, Appl1
37	152	10.2	320	4 US-08-205-697A-2	Sequence 2, Appl1
38	152	10.2	320	4 US-08-702-525-2	Sequence 2, Appl1
39	152	10.2	320	5 PCT-US95-02576-2	Sequence 2, Appl1
40	151.5	10.1	306	4 US-08-205-697A-17	Sequence 17, Appl1
41	151.5	10.1	306	4 US-08-702-525-17	Sequence 17, Appl1
42	151.5	10.1	306	5 PCT-US95-02576-17	Sequence 17, Appl1
43	147	9.8	342	2 US-08-724-394A-6	Sequence 6, Appl1
44	144.5	9.7	306	2 US-08-147-772-4	Sequence 4, Appl1
45	144.5	9.7	306	2 US-08-456-104-8	Sequence 8, Appl1

ALIGNMENTS

RESULT 1
US-08-456-104-4
; Sequence 4, Application US/08456104
; Patent No. 5861310
; GENERAL INFORMATION:
; APPLICANT: Freeman, Gordon J.
; APPLICANT: Nadler, Lee M.
; APPLICANT: Gray, Gary S.
; TITLE OF INVENTION: TUMOR CELLS MODIFIED TO EXPRESS B7-2 AND B7-3 WITH INCREASE
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESS: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,104
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/101,624;
; FILING DATE: 26-JUL-1993;
; APPLICATION NUMBER: 08/109,393;
; APPLICATION NUMBER: 19-AUG-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: RPI-008
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 227-5941
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-456-104-4
Query Match 12.2%, Score 182; DB 2; Length 309;
Best Local Similarity 23.6%, Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;

US-08-479-744A-23
Sequence 23, Application US/08479744A

12.2%; Score 182; DB 3; Length 309;

RESULT 3
US-08-280-757B-23
; Sequence 23, Application US/08280757B

US-08-280-757B-23

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Query Match 12.2%; Score 182; DB 4; Length 309;
Best Local Similarity 23.6%; Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;

OY 7 GLLFLTFSS--LRADTOKEVRAMWGSDELSCACPEGSREDLNDVYYWQTSSEKTYVT 64
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 8 GLALLIFVYVLLIDDAVSVEIQALFNGAIYLPCEFTKAKNLSISELYVFWO--DOAKLY 66
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 65 YHIDPNSLENDVSRYYRRNALMSPAGMLRGDFSRLFNVTPODEOKFHLVLSQ---SL 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 67 EHYIGTEKLDVSNNAKYLCRTSFD-----RNWMTLRHLHWQIKDMSGDCEIQKKRPTGSI 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 121 GFOEVLSEVYTLHVAANSPVYVS-APHSPQDEDLFTFCTSLNGVPRP-NYYWL--NKT- 175
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 122 ILQQLTL---ELSYIANSEPEIKLAQVTVGNSGILNLTCSKQHPKPKMYFLITNSTN 178
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 176 ---NSNLLDQALQNDTVFELNKRGLDYVSVLRIARTPSV---NTGCCIEENLLQONLTVG 229
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 EYGDWMOQISQO-----NTVELFISINLSLSPPDGVMMHTVVCVELT---ESMKIS 226
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 230 SQTGNDIGERKTKTENPVSTGEKNAATWSILLAVLCCLVYVAVALGWCRDCLQHS 285
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 227 SKPLNFTGE---FPPSPQTYWKETIASVYVALLVLLMLLI-----VCHKRPNPS 272
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 4
US-08-205-697A-21
Sequence 21, Application US/08205697A
Patent No. 6218510
GENERAL INFORMATION:
APPLICANT: Sharpe, Arlene H.
APPLICANT: Borriello, Francescopaulo
APPLICANT: Freeman, Gordon J.
APPLICANT: Nadler, Lee M.
TITLE OF INVENTION: No. 6218510e1 Forms of T Cell Costimulatory Molecules
TITLE OF INVENTION: and Uses Therefor
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESS: LAHIVE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697A
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: BWI-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-205-697A-21

Query Match 12.2%; Score 182; DB 4; Length 309;
Best Local Similarity 23.6%; Pred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14;

7 GLLFLTFSS--LRADTOKEVRAMWGSDELSCACPEGSREDLNDVYYWQTSSEKTYVT 64

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Db	8	GLAIIIFVYLLISDAVSEVQAFNGFATVLPCEPFTKAQNIISLSELVEMQ--DQCKLV	66
Qy	65	YHLPQSSLENDSCRKRRPALMSRPMGRGSELRLENVTPROBEOKFHCLVLSQ----	SL 120
Db	67	EHVIGTEKLDVNAKLTGSTSD-----RNWTLIRLHNQIKMGSSDYCEIQKRPPTGI	122
Qy	121	GFOEVLSEVETLHVANSEVPVVS-APHSPODELTFTCSINGYRP--NVYMI--NKT-	175
Db	122	ILQOFTL---ELSVIANESEPEIKLAQNVTSNGSINLTCSKGQHPKPKMYFLITNSTN	176
Qy	176	---DNSLIDQALQNDTVFLNMKGVDVYSVIRPDSV---NGGICFNVLLQONLVG	228
Db	179	EYGDNQIISD-----NVTLEFSINSLSLSPFGVHMKTVVCULET-----ESMKIS	228
Qy	230	SQGNIDIGERDKTENPVSSTGKRNATWSILAVLCILLVVAALIGWCSDROLQHS	285
Db	227	SKPLNFTQE---FSPSPQYVMEKTIASVYALLVMLLI-----VCHRRKNQPS	272

```

RESULT 5
US-08-702-525-21
; Sequence 21, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E,
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BMT-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 309 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-21

Query Match      12.2%; Score 182; DB 4; Length 309;
Best Local Similarity 23.6%; Fred. No. 3e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14,

QY      7 GLPLFLFS--LRADTQEKREVRAMWGSDVETSCACPEGSRFPDINDVYYWQTSSEKTYVT 64
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||::
DB      8 GLAIIIFTVVLISDAVSVEIOTAYFNNGRAYLFCPTTKAONISLSSELVFWQ--DQOKLYLV 66

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Db      232 SKPLNFTQE-----PSPDQYWKMETASTAYTVALLLVLLIT-----VCHKKRPNQPS 277

RESULT 8
US-08-702-525-13
; Sequence 13, Application US/08702525
; Patent No. 6294660
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; APPLICANT: Borriello, Francescopaolo
; APPLICANT: Freeman, Gordon
; APPLICANT: Nadler, Lee
; TITLE OF INVENTION: No. 6294660el Forms of T Cell Costimulatory
; TITLE OF INVENTION: Molecules and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; City: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,525
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 314 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-702-525-13

Dry Match      12.2% Score 182; DB 4; Length 314;
Best Local Similarity 23.6% Pred. No. 3,1e-10;
Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14.

Db      7 GLLFLFSS--LRADTQEKVRAMGSDVEISCACPBESSRFDLNDVYVYVWQTSSEKTVMT 64
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      13 GLAILLFVTVLLISDAVSVETQAVYNGTAYLPCPTTKAONISLELVFWQ--DQOKLVLT 71
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      65 YHLPONSLENVDSRRNRNALMSPAGMLRGDPSLPLFVYTPDQDKHCVLSQ---SL 120
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      72 EHYTGTEKLDYSVAKVLGRTSFD-----RNMTTLRLHNVQIKDMSGYDCLQKKRPPTGSI 126
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121 GFOEVLSEVETTLVAFANFSVPYVS-APHSPODELTFTCTISNGYPRP-WVYWI--NKT- 175
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      127 ILQQTLL---ELSVIANFSEPEKTLAQNVTGSGINLCTSKQGHPRPKMYFLINSTN 183
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      176 ---DNSLLDQALONDFVILNMRGLYDVVSYLEIARTPSV---NIGCCIEVLLQDNLTVG 229
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      184 EYGDNMQISD-----NVTLEFSISNLSLSLSPDGVWMTVVCLET-----ESMKIS 231
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      230 SQGNQDGEEDKRTENPVSTGEKNATMSILAVLCLLVYVAVALGWCRCRQIOHS 285
      11 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      232 SKPLNFTQE-----PSPDQYWKMETASTAYTVALLLVLLIT-----VCHKKRPNQPS 277

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```

      RESULT 9
      PCT-US95-02576-13
      Sequence 13, Application PC/TUS9502576
      GENERAL INFORMATION:
      APPLICANT:
      TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
      TITLE OF INVENTION: and Uses Therefor
      NUMBER OF SEQUENCES: 65
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: LAHIVE & COCKFIELD
      STREET: 60 State Street, suite 510
      City: Boston
      STATE: Massachusetts
      COUNTRY: USA
      ZIP: 02109-1875
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: ASCII text
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: PCT/US95/02576
      FILING DATE:
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 08/205,697
      FILING DATE: 02-Mar-1994
      ATTORNEY/AGENT INFORMATION:
      NAME: Mandragouras, Amy E.
      REGISTRATION NUMBER: 36,207
      REFERENCE/DOCKET NUMBER: BWT-120CPC
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (617)227-7400
      TELEFAX: (617)227-5941
      INFORMATION FOR SEQ ID NO: 13:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 314 amino acids
      TYPE: amino acid
      TOPOLOGY: linear
      MOLECULE TYPE: protein
      PCT-US95-02576-13

      Query Match      12.2%; Score 182; DB 5; Length 314;
      Best Local Similarity 23.6%; Pred. No. 3,1e-10;
      Matches 70; Conservative 61; Mismatches 117; Indels 48; Gaps 14.

      Oy      7 GLEFLRSS--LRADQKEKVRAMGSDVELSCAPESRDLNDVYVWQTSSESKYV 64
      Db      13 GLAILIFVALLISDAVSVETQAVENGTAIVLRCPRTKAQNISLSELVFWO--DQKLVLT 71
      Oy      65 YHIQNSSLINVSVRARNRLMSPAGMLRGDFSLRFLFVTFQDEQKFCVLVSQ---SL 120
      Db      72 EHYIYCTEKLDISVAKYIGRTSP-----RNMTLTLLHNVQIKDWSYDCFIQKKRPITGI 126
      Oy      121 GEQVLSVEVTLVHANFSVYVVS-APHSPSODELTFCTCSINGYPRP-NVYWT--NKT* 175
      Db      127 ILQQTIF---ELSYIANFSEPEIKILAQNVYTGSGINTLCTSKQGHPRKMYFLITNSTN 183
      Oy      176 ---NSNLLDQALQNDYFLNMRGLNYVVSVLRIATPSV---NIGCCLENVLLQQNTVG 229
      Db      184 EYGNMQISD-----NVTELFISINSLSLSPDGVGMHMYVAVLET---ESMKIS 231
      Oy      230 SQTNDNGEDRKITENPVSTGEKNATWSILAVLCLLVVAIVAIGWCRDCLQHS 285
      Db      232 SKPLNFTQE---FPSPQTYWKEITASTSYVALLLVMLLTI-----VCHKKRPNPS 277

      RESULT 10
      US-08-724-394A-1
      Sequence 1, Application US/08724394A
      GENERAL INFORMATION:
      APPLICANT: Feder, John N.

```

```

: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Purified Mammalian CTLA-4 Binding
: TITLE OF INVENTION: Protein and Related Reagents
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Schering-Plough Corporation, M-3-W
: STREET: One Giralda Farms
: CITY: Madison
: STATE: New Jersey
: COUNTRY: USA
: ZIP: 07940-1000
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: Apple Macintosh IIcx
: OPERATING SYSTEM: System Software 7.1
: SOFTWARE: Microsoft Word 5.1a
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/09642
: FILING DATE:
: CLASSIFICATION:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/120,606
: FILING DATE: 13-SEP-1993
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/116,882
: FILING DATE: 03-SEP-1993
: ATTORNEY/AGENT INFORMATION:
: NAME: Blasdale, John H. C.
: REGISTRATION NUMBER: 31,895
: REFERENCE/DOCKET NUMBER: DX0390K1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 201-822-7039
: TELEFAX: 201-822-7039
: INFORMATION FOR SEQ. ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 323 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: PCT-US94-09642-2

Query Match 11.1%; Score 165.5; DB 5; Length 323;
Best Local Similarity 21.7%; Pred. No. 1.4e-08;
Matches 65; Conservative 61; Mismatches 121; Indels 53; Gaps 13,

QY 3 LGSGLLEFLFSRLADTQEKERVAMVSGDVELSCAPESGRFDLNVYYWQTSKTY 62
Db 1 MGSNLTLEFV-APLLSGAAPLKTIQAFNEFADLPQCFANSONOSLSLTVFMWDOQENLV 59
QY 63 VYHIIPNSSLLEVNDSDRYRNRLAMPAGMLRDFSLRLFNVTPODEQKFNCLV-LSOSIG 121
Db 60 NEVYLGG-EKFDSDVHKYKMGRTSPD-----SDSWTLRLHNIQIDKDLVYCITIIHHKPPG 113
QY 122 FQEVLSYEVTTLHYAANFVSP-VYSAPHSPSODELTFCTGSINGYPRP-NVYMWINKTDSL 179
Db 114 MIRHQNNSELVLANFSGPEIIVPISNTENYINLTCSSIHGYEPBKMSVLLRTKNSGT 173
QY 180 LD-----QAQNDVTYVLNKRGLYDVVSLRKA---RTPSVNIGCCITNVLLOQNLTVGSG 231
Db 174 IEYDGMQNSQD-----NVTLEYDISLSVSPFDVYSNMRTIFILET----- 216
QY 232 TGNDIGGRKITEPNVSTGEKNA-----ATWSILAVL-----CLLVAVVAVALGWCCRDR 280
Db 217 -----DKTRLSSPFSITLEDPPPPDHIFW-ITAVLPYVIICVMVFCILIMKKKKRR 269

RESULT 12
US-08-456-104-2
: Sequence 2, Application US/08456104
Patent No. 5861310
GENERAL INFORMATION:
APPLICANT: Freeman, Gordon J.

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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 23 Oct 102 14:25:42-PDT

Solution Parameters:

Amino Alphabet = Identity
Output line length = 80
Compress = Off
Histogram = Off
Randomization = Off
AMINO-Res-length = 2
Deletion-weight = 5.00
Length-factor = 0
Matching-weight = 1.00
CLIC-Res-length = 4
Spread-factor = 50

Clustered order of selected sequences:

13. US-09-728-420C-17 (1-302)
14. US-09-728-420C-18 (1-302)
9. US-09-728-420C-12 (1-288)
10. US-09-728-420C-13 (1-267)

Region Alignment: (listed in Clustered order)

US-09-728-11 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-18 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-12 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
US-09-728-13 1 MRGSPGLFLFLFSSLRADTQEKVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
EKEVRAWGSVDVLSQACPEGSRFDLNDVYVYVWQTSSEKT
consensus mrlgspglflflfsslradtqekvramwgsdvlsqacpegsrfdlndvyvyywqtseskt

US-09-728-62 VVTYHLPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLFNVTPODEQKFHCLVLSQSLGF
US-09-728-62 VVTYHLPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLFNVTPODEQKFHCLVLSQSLGF
US-09-728-62 VVTYHLPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLFNVTPODEQKFHCLVLSQSLGF
US-09-728-41 VVTYHLPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLFNVTPODEQKFHCLVLSQSLGF
consensus VVTYHLPQNSSLENDVSRYNRRALMSPAGMLRGDFSLRLFNVTPODEQKFHCLVLSQSLGF

US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-123 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
US-09-728-102 QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA
consensus QEVLSVEVTLHVAANFSPVVSAPHSPODELFTCTCSINGYPRPNVYWIINKTDSILLDOA

US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE
US-09-728-184 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE
consensus LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE

US-09-728-163 LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE
consensus LQNDTVFLNMRGLYDVVSVLRIARTPSVNIACCIEENVLLQONLTVGSQGTGNDIGERDKITE

US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRDRCLOHSHYAGAMAVSPETELTGHV
US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRDRCLOHSHYAGAMAVSPETELTGHV
US-09-728-245 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRDRCLOHSHYAGAMAVSPETELTGHV
US-09-728-224 NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRDRCLOHSHYAGAMAVSPETELTGHV
consensus NPVSTGEKNAATWSILAVLCILVYVAVAIGWVCRDRCLOHSHYAGAMAVSPETELTGHV

Alignment score = 612.00

Scoring matrix:

	9	10	13	14
9	162	218	218	
10		92	92	
13			302	
14				

